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RESULT 1 September 29, 2003, 08:01:08; Search time 44 Seconds (without alignments) 1111.086 Million cell updates/sec US-10-088-548-2 1786 1 KSPVVQDCYHGDGRSYRGIS......YTMNPRKLFDYCDIPLCASS 308 /SIDS1/qcgdata/geneseq/geneseqp-emb1/AA2003.DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT;* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT;* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT;* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000. embl/AA1999 'gcgdata/geneseg/genesegp-emb1/AA2001 -embl/AA199 SIDS1/gcgdata/geneseq/genesegp-emb1/AA199 /SIDS1/qcgdata/geneseq/genesegp-emb1/AA1981 944443 /qcqdata/qeneseq/qeneseqp-emb1/AA19 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. /gcgdata/geneseq/genesegp-embl 'SIDS1/gcgdata/geneseq/geneseqp SIDS1/gcgdata/geneseq/geneseqp 'SIDS1/gcgdata/genesegp/genesegp 'SIDS1/gcgdata/geneseg/genesegp SIDS1/gcgdata/geneseg/genesegp /gcgdata/geneseg/genesegp otal number of hits satisfying chosen parameters: 1107863 segs, 158726573 residues ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries I protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 A_Geneseq_19Jun03:* /SIDS1 SIDSI .nimum DB seq length: 0 wimum DB seq length: 308 SIDSI ttle: erfect score: coring table: tabase : sarched: :eouenbe : ao u

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human angiogenesis	Human plasminogen	Human plasminogen	A multifunctional	A multifunctional	Bovine kringle 1-3	Porcine kringle 1-	A multifunctional	A multifunctional	
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	227.0 227.0 26.5 26.5 26.5 26.5

ALIGNMENTS

Human, angiogenesis inhibitor; LK68; apolipoprotein(a) kringle domain; angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy; cytostatic; antirheumatic; antiarthritic; antipsoriatic; psoriasis; ocular angiogenic disease; endothelial cell proliferation; tumour; /label= KIV36 /note= "Apolipoprotein(a) kringle domain IV36, LK6 119..207 Alabel= KIV37 ^note= "Apolipoprotein(a) Kringle domain IV37, LK7 protein" 223..308 //label= KW38 protein" protein" Human angiogenesis inhibitor, LK68 protein. Location/Qualifiers AAY72944 standard; Protein; 308 AA (first entry) rotein" cell migration Homo saplens 13-JUN-2001 AAY72944; Key Domain Domain Domain

WO200119868-A1

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King protein contains the amino acid sequences of human apolipoprotein(a) kringle domains IV36 (LK6 protein), IV37 (LK7 protein) and V38 (LK6 protein), LK68, LK7, LK7 and LK8 are inhibitors are of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo chorioallantoic membrane (CAM). LK68 protein, its single kringles or their functional equivalents, are useful for treating anglogenesis-mediated diseases, such as cancer, rheundroid arthritis, psoriasis or coular anglogene disease in animals or humans. LK68 is useful as an anticancer agent and also for inhibiting primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSGKQPWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVR 120
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                                                                                                                                                                                                                                                                            Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KSPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is human angiogenesis inhibitor, LK68 protein.
                                                                                                                                                                                                                                                                                                apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid sequence
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                                                                                                                                                                                     Yum J, Chung S;
                                                                                                                                                  (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
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                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 42-44; 50pp; English.
                                                                                                                                                                                     Chang J, Kim JS, Park EJ,
                                                                           99WO-KR00554
                                                                                                            99WO-KR00554
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                                                                         15-SEP-1999;
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                                     22-MAR-2001
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Gaps

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The invention relates to a method of preparing plasminogen kringle 5

peptide fragments. The method comprises mixing mammalian plasminogen and
elastase in the ratio 1.100-1.300, followed by incubating and isolating
the fragment. The kringle 5 peptides are inhibitors of angiogenesis and
endothelial cell proliferation and migration. The peptides are useful
for treating angiogenic diseases, primary and meterstratic solid tumours
and carcinomas of various organs such as breast, genital tract,
endocrine glands, skin, tumours of the brain and eyes and solid tumours
and carcinomas of various organs such as leafwaemias and
lymphomas. They are also used for the prophylaxis of various autoimment
diseases (e.g., rheumatoid arthritis), cular diseases, skin diseases
conforme), diseases caused by excessive or abnormal stimulation of
endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases
conforthelial cells (e.g., Crohn's disease, atherosclerosis), diseases
conforthelial cells (e.g., voultation and establishment of the placenta.
Conforms AbB01906-B01919 represent fragments of human plasminogen used
in an exemplification of the invention.
Note: This sequence is not shown in the specification, but is derived
from the full length human plasminogen sequence (ABB01887) shown in
                                   Plasminogen; human; Kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiatrefroscierrotic; cytostatic; antiprolifematory; antiuloer; antitheumatic; antiatric; antianglogenic; cancer; tuncur; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GPWCFTTDPSVRWEYCNIKKCSGTEASVVAPPPVVLLPDVETPSEEDCMFGNGKGYRGKR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 ATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation of Kringle five peptide fragment for treating various disorders such as anglogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Human plasminogen kringles 4-5 (Val355-Ala543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                              96US-0643219.
97US-0832087.
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Matches 150; Conservative
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                                                                                                                                                                                                                                                           05-MAY-1997;
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                   03-APR-1997;
                                                                                                                                                                            US6057122-A.
                                                                                                                                                                                                                                                                                              03-MAY-1996;
                                                                                                                                                                                                                     02-MAY-2000,
                                                                                                                                                                                                                                                                                                                                                                                                  Davidson DJ;
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The invention relates to a method of preparing plasminogen kringle 5

peptide fragments. The method comprises mixing mammalian plasminogen and
elastase in the ratio 1100-1300, followed by incubating and isolating
the fragment. The kringle 5 peptides are inhibitors of anglogenesis and
endothelial cell proliferation and migration. The peptides are useful
for treating anglogenic diseases, primary and metastatic solid tumours
and carcinomas of various organs such as breast, gential tract,
and carcinomas of various organs such as breast, gential tract,
and carcinomas of various organs such as breast, gential tract,
and carcinomas of various organs such as breast gential tract,
and carcinomas. They are also used for the prophylaxis of various autoimmune
lymphomas. They are also used for the prophylaxis of various autoimmune
diseases (e.g., rheumatoid arthritis), coular diseases, skin diseases
(e.g., psoriasis), blood vessel diseases (e.g., heamangiomas, obler Webber
Sydrome), diseases caused by excessive or abnormal stimulation of
endothellal cells (e.g., croin's disease, atherosolerosis), diseases
which have angiogenesis as a pathologic consequence (e.g., cat scratch
agent which inhibits ovulation and establishment of the placenta.

Sydromes Aabolgo6-Bolgig represent framents of human plasminogen used
in an exemplification of the invention.
                                                                                                                                                                                                                         angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antiproliferative; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                         Plasminogen; human; kringle domain; endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.1%; Score 913; DB 21; Length 192; 79.4%; Pred. No. 1.3e-51; tive 17; Mismatches 22; Indels (
                                                                                                                                                                Human plasminogen kringles 4-5 (Val355-Phe546).
                                      AAB01919 standard; Protein; 192 AA.
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Best Local Similarity 79.44
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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03-APR-1997;
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                                                                                                                     18-SEP-2000
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                                                                             AAB01919;
RESULT 3
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combinations of anglostatin, andstatuble proteins willow comprise combinations of anglostatin, and platelet factor, thrombospondin, interferon.inducible protein and platelet factor 4, and have anti-anglogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverses side effects, or a combination of these properties. The proteins can be used for treating an anglogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, growth. The present sequence represents a multifunctional protein of the invention.
                                                                        61 GPWCFTTDPSVRWEYCNIKKCSGTEASVVAPPPVVLLPDVETPSEEDCMFGNGKGYRGKR 120
                                                                                                                                        179 GPWCFTIDPSIRWEYCNLIRCSDIEGTVVAPPIVIQVPSLGPPSEQDCMFGNGKGYRGKK 238
                                                                                                                     239 ATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYIWNPRKLFD 298
                 9
New multifunctional proteins useful for treating angiogenic-mediated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes multifunctional proteins which comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casperson GF, Gregory SA;
                                                                                                                                                                                                                                                                                                                                                                                                                           A multifunctional protein of the invention.
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                                                                                                                                                                                                                                                                                                                   AAY02108 standard; Protein; 280 AA.
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Klein BK, McKearn JP;
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181 YCDVPQCAA 189
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                                                                                                                                       159
                                                                             PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHG 125
                                                                                                                   NGQSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMMYCRNPDADIGPWCFTT 185
                                                                                                                                                                                               242 VTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCD 301
                                                                                                                                                                                                         63
                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes multifunctional proteins which comprise combinations of anglostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-anglogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater
                                                                                        64 PWCFTIDPNKRWELCDIPRCT-----TPPPS-----YQCLKG
                                                                                                                               DPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPS----EQDCMFGNGKGYRGKKATT
                                                                                                                                                                     6 QDCTHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQ
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                  Angiostatin; endostatin; interferon; thrombospondin;
interferon inducible protein; platelet factor 4; anti-angiogenic;
anti-tumor; multifunctional protein; angiogenic-mediated disease;
cancer; diabetic retinopathy; macular degeneration; arthritis;
                    36;
Length 280;
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregory
 DB 20;
                                                                                                                                                                                                                                                                                                                                                               A multifunctional protein of the invention.
                    40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Casperson GF,
41.7%; Score 744; 42.7%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New multifunctional proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 99-100; 121pp; English
                                                                                                                                                                                                                                                                                                       AAY02103 standard; Protein; 297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US20464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97us-0060609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caparon MH,
                                                                                                                                                                                                                                                                                                                                            (first entry)
                   Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bolanowski MA, Caparo
Klein BK, McKearn JP;
                                                                                                                                                                                                                                                                                                                                                                                                                          tumor cell production
                                                                                                                                                                                                                                                 : |: :
LKKCSGT 278
                                                                                                                                                                                                                                    302 IPLCASS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-255098/21.
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SEAR ) SEARLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                            16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9916889-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                             99
                                                                                                                                                         186
                                                                                                                                                                           160
                                                                                                                                                                                                                                                      272
                                                                                                                                                                                                                                                                                                                        AAY02103;
 Query Match
           Best Local
                                                                                                                                                                                                                                                                                              AAY02103
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66 PWCYTIDPCVRWEYCNLIQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PWCFTIDPNKRWELCDIPRCT-----TPPPS-----SGPT-----YQCLKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 NGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCFTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VIGIPCQEWAAQEPHRHSIFIPGINKWAGLEKNYCRNPDGDINGPWCYIMNPRKLFDYCD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an anniquent-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatcma, sarcoma and lymbóma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 NSQVRWEYCKIPSCDS-----SPVSTEQLAPIAPPELTPVVQDCYHGDGQSYRGISSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 QDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPS----EQDCMFGNGKGYRGKKATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                               Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                        41.7%; Score 744; DB 20;
42.7%; Pred. No. 1.6e-40;
live 40; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW07570 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US05856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0612788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960S-0605598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 42.7 tes 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 IPLCASS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKCSGT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-518662/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine kringle 1-3.
                                                                                                                                                                                                                                                                                                                                                   297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1996;
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The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 1, kringle 1-3, kringle 1-3, kringle 1-4 or kringle 1-4 bKLS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or approximately amino acid number 98 of murine, an beused for treating and openeration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, bovine kringle 1-3, is a specific angiostatin fragment which can be used in the invention, and represents amino acids 6-255 of bovine angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GOSYRGTESTTVTGRTCQSWSSMTPHRAQRTPENYPNDGLTMNYCRNPDADTGPWCFTTD 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CYHGDGRSYRGISSTTVJGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ-P 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.1%; Score 716; DB 17; Length 250; Best Local Similarity 42.1%; Pred. No. 8.6e-39; Matches 126; Conservative 43; Mismatches 80; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW07569 standard; protein; 250 AA
                                                                            Claim 4; Page 128; 203pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US05856.
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95US-0429743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine kringle 1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA;
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26-APR-1995;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 WCYTTDPETRFDYCDIPECED------ECMHCS 87
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragment, a combination of angiostatin fragments, or human, Rhesus, porcine or bovine plasminogen and is a kringle 1-2, kringle 2, kringle 1-3, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-4, kringle 1-4, kringle 1-2, kringle 1-4, kringle 1-2, kringle 1-6, kringle 1-4, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-4, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-4, kringle 1-2, kring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSG-KQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CKTGNGKNYRGTTSKTKSGVICQKWSVSSPHIPKYSPEKFPLAGLEENYCRNPDNDEKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 715; DB 17; Length 250;
42.5%; Pred. No. 1e-38;
tive 41; Mismatches 81; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies for use in diagnosis, detection and therapy.

The present sequence, porcine kringle 1-3, is a specific angiostatin fragment which can be used in the invention, and represents amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC
                                                                                                                                                                                                                                                                  endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                      Use of angiostatin fragments or aggregates - for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angiostatin; endostatin; interferon; thrombospondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A multifunctional protein of the invention.
                                                                                                                   Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 126-127; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids 6-255 of porcine angiostatin.
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                                                     (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                   Cao Y, Folkman MJ, Lin J,
96US-0605598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 127; Conservative
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                                                                                                                                                                              WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 AA;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1999
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9

A multifunctional protein of the invention.

(first entry

16-JUL-1999

AAY02102;

AAY02102 standard; Protein; 285 AA.

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The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 QCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECMHCSGENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCFTTDPSIRWEYCNLTRCSDTEGIVVAPPIVIQVPSLGPPSEQDCMFGNGKGYRGKKAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 WCFTTDPNKRWELCDIPRCT-----TPP-----PSSGPTYQ--CLKGTGENYRGNVAV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGKQ-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SPVVQDCYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVILSECKTGNGKNYRGTMSKTKNGITCQKWSSISPERPRFSPATHPSEGLEENYCRNPD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.9%; Score 713; DB 20; Length 268; 42.2%; Pred. No. 1.4e-38; ive 41; Mismatches 87; Indels 5
                                                                                                                                                                                                                                                                 Gregory SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | ||||||||| |::||::| | 62 NDPQGPWCYTTDPEKRYDYCDILECEE------
                                                                                                                                                                                                                                                                 Casperson GF,
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 104; 121pp; English.
                                                                                                                                                                                                                                                                 Caparon MH,
                                                                                                                                                                                 97US-0060609
                                                                                                                                          98WO-US20464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 130; Conservative
                                                                                                                                                                                                                        (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                  McKearn JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 KIPSCDSS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 DIPLCASS 308
                                                                                                                                                                                                                                                                                                                           WPI; 1999-255098/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 AA;
                                                                                                                                                                                                                                                                 Bolanowski MA,
                     Homo sapiens.
                                                                                                                                                                                 01-OCT-1997;
                                                          WO9916889-A1
                                                                                                                                          30-SEP-1998;
                                                                                                 08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
                                                                                                                                                                                                                                                                                      Klein BK,
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Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon.inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic and confidence as an engineering and activities. The proteins can be used for treating the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, remal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGKQ-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 SVYLSECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRESPATHPSEGLEENTCRNPD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| i :| i | i | i | i | i | i | ECMECSGENYDGKISKIMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRELRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New multifunctional proteins useful for treating anglogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.9%; Score 713; DB 20;
42.2%; Pred. No. 1.5e-38;
ive 41; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Casperson GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 97-98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MA, Caparon MH,
McKearn JP;
                                                                                                                                                                                                                                                                                                                                     98WO-US20464
                                                                                                                                                                                                                                                                                                                                                                     97us-0060609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 42.2
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-255098/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolanowski MA,
                                                                                                                                                                                                                                                                                                                                     30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1997;
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                       W09916889-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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RESULT 9 AAY02102

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The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., rbeumatoid arthritis), ocular diseases, skin diseases (e.g., pood vessel diseases (e.g., haemangiomas, osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of
                                                                                              angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antiproliferative; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                              184 ITDPSIRWEYCNLIRCSDIEGIVVAPPIVIQVPSLGPPSEQDCMFGNGKGYRGKKAIIVT 243
                                                                                                                                                                                150 TIDPNKRWELCDIPRCT----TPP----PSSGPTYQ--CLKGIGENTRGNVAVIVS 195
                                                                                                                                                                                                                   244 GIPCQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIP 303
 65 Q-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCY 123
                                                                         124 HGNGQSYRGTFSTIVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADTGPWCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; human; kringle domain; endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                     Human plasminogen kringles 1-3 (Tyr80-Pro353).
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB01910 standard; Protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 17; Page -; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0851350.
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                                                                                                                                                                                                                                                                                            304 LCASS 308
                                                                                                                                                                                                                                                                                                                              254 SCDSS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1996;
03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB01910;
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                       AAB01910
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                                  g
                                                                         QY
                                                                                                     g
                                                                                                                                              QΫ́
                                                                                                                                                                                  g
                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                              셤
                                                           This sequence represents kringle domains 1-3 of human plasminogen. A 38 harterminal fragment of plasminogen is referred to as angiostatin and inhibits neovascularisation. Angiostatin contains 4 kringle domains of the parent molecule. However, angiostatin containing all 4 kringle domains of the parent molecule. However, angiostatin containing all 4 kringle domains (KI-4) was found to be no more potent as an inhibitor of cell proliferation than an angiostatin only containing KI-3. Therefore, kringle 4 does not posses inhibitory activity. A fragment of the plasminogen coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably angiostatin. The vector, which may be a replication defective viral vector, is useful for inhibiting angiogenesis in a mammal, especially
166 WCFTIDPNKRWELCDIPRCT-----TPP-----PSSGPTYQ--CLKGTGENYRGNVAV 211
                                    241 IVIGIPCQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYIMNPRKLFDYC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VODCYHGDGRSYRGISSITVTGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant viral vector expressing human angiostatin useful for inhibiting angiogenesis in a mammalian subject with cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.9%; Score 712; DB 24; Length 260; 42.3%; Pred. No. 1.6e-38; Live 41; Mismatches 85; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                    Human; plasminogen; angiostatin; neovascularisation;
kringle domain; cell proliferation; viral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jooss K,
                                                                                                                                                                                                                                                                                                                                                  Human plasminogen kringle domains 1-3, K1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 75-76; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       replication-defective; cancer; tumour.
                                                                                                                                                                                                                                      AAG79748 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu WW, Macarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-2002; 2002WO-US13461.
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                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with cancer or a tumour
                                                                                                             301 DIPLCASS 308
                                                                                                                                              270 KIPSCDSS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-129131/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABA00776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200288173-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                             18-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                           AAG79748;
                                                                                                                                                                                                     ESULT 10
                                                                                                                                                                                                                     AG79748
D AAG7
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regions of plasminogen linked to the glycosylated form, useful for inhibiting angiogenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Madsen J, Liang H, Sim KL, Zhou X, C
Bermejo LL, Mistry FR, Schrimsher JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU01209 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Angiostatin (hASv3) protein.
                                                        Claim 7; Fig 1; 42pp; English.
                                                                                                                                                                                                                                   Ouery Match 39.8%;
Best Local Similarity 42.3%;
Matches 129; Conservative 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2000; 2000WO-US32843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0168919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ENTR-) ENTREMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 LCASS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 SCDSS 258
                                                                                                                                                                                                   260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70200140260-AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01209;
                                                                                                                                                                                                     Sedneuce
                                                                                                                                                                                                                                       Query Match
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     QΫ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                 65 Q-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 TIDPSIRWEYCNLTRCSDIEGTYVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ECM 88
                                                                                                                                                                                                                                                                                            64
endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AAB01906-B01919 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                 149 TIDPNKRWELCDIPRCT-----TPP-----PSSGPTYQ--CLKGTGENYRGNVAVTVS
                                                                                                                                                                                                                                                                                            5 VQDCYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                   124 HGNGQSYRGTFSTIVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCF
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition comprising deglycosylated fragments of kringle 1-5
                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sim
                                                                                                                                                                                                                    Length 274;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MacDonald
                                                                                                                                                                                                                  Score 712; DB 21;
Pred. No. 1.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deglycosylated; kringle; angiogenesis; human
                                                                                                                                                                                                                                                      41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deglycosylated kringle 1-5 region protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liang H,
                                                                                                                                                                                                                                                                                                                                                                                    62 QGPWCYTTDPEKRYDYCDILECEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB26486 standard; Protein; 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ENIR-) ENTREMED INC. (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pirie-Shepherd S, Folkman MJ,
                                                                                                                                                                                                                  39.9%;
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99US-0128062.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                        Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-579032/54
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 LCASS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 SCDSS 257
                                                                                                                                                                                274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA94906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1999;
07-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2000
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB26486;
                                                                                                                                                  figure 1.
                                                                                                                                                                                                                      Query Match
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          65 Q-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCY 123
                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                       GTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIP 303
                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                     89
The present sequence is deglycosylated kringle 1-5 region protein. Deglycosylated kringle 1-5 region protein has increased antiangiogenic activity as compared to glycosylated kringle 1-5 region protein. The deglycosylated kringle 1-5 region protein was isolated from human plasminogen by affinity chromatography.
                                                                                                                                                                                                   124 HGNGQSYRGIFSTTVTGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDADIGPWCF
                                                                                                                                                                                                                                                                                                                                                              TIDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVT
                                                                                                                                                                                 5 VQDCYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGK
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Angiostatin; recombinant production; cation exchange column; fermentation; anglogenesis mediated disease; leukaemia; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.J.;
                                                                                                                                                     20;
                                                                                                                       Length 260;
                                                                                                                       ; Score 711; DB 21; Length 26; Pred. No. 1.9e-38; 40; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang-Murad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; plague neovascularisation.
                                                                                                                                                                                                                                                                         63 QGPWCYTTDPEKRYDYCDILECEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-408277/43.
N-PSDB; AASO4181.
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Purifying recombinant angiostatin, involves applying fermented containing angiostatin to expanded bed cation exchange column, exchange column, hydroxyapatite column, hydrophobic column and
                                         Example 1; Page 22; 49pp; English.
                                                                                                                                                                                                      liquid or frozen, or lyophilised
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AA; Sequence

149 TIDPSIRWEYCULTRCSDIEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVT 243 124 HGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRIPENYPNDGLTMNYCRNPDADTGPWCF 183 GTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIP 303 65 Q-PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCY 123 62 89 QGPWCYTTDPEKRYDYCDILECEE------ECM 5 VQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLIENTCRNPDSGK 50; 39.8%; Score 711; DB 22; Length 260; 42.3%; Pred. No. 1.9e-38; tive 40; Mismatches 86; Indels 5 Conservative Local Similarity les 129; Conserv 304 LCASS 308 SCDSS 258 90 184 196 254 Query Match Matches

ESULT 14 AY53869

Kim Y, 39.6%; Score 707; DB 21; 42.4%; Pred. No. 3.3e-38; Live 40; Mismatches 84; Jung S, Claim 2; Page 47-48; 55pp; English. Lee H, (GREC) KOREA GREEN CROSS CORP 98KR-0019535, 99KR-0019144. 99WO-KR00263. Query Match 39.6 Best Local Similarity 42.4 Matches 128; Conservative Ahn BC, WPI; 2000-086703/07 So SH, A Chang S; 254 AA; AS 307 28-MAY-1999; 28-MAY-1998; 27-MAY-1999; 02-DEC-1999 186 83 306 Sequence diseases You WK, Joe YA, 쉱 δy g δ g δŽ g δŽ D, ð The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production. Tecovery and purification of Angiostatin protein. Purification of recombinant Angiostatin comprises applying crude fermentation broth containing the Angiostatin comprises applying crude fermentation broth containing the process of protein to an expanded bed cation exchange column, eluting it, and a paplying the elutate to anion exchange column, repeating the process of eluting and applying, to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiogenesis mediated diseases, including solid tumours, lenkaemia, tumour metastases, benign tumours, Including solid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber syndrome, myocardial angiogenesis, plaque necovacularisation, telangiectasia, haemophiliac joints, angiofibroma and wound granulation. As a centrifugation technique is not employed in the process, damage to the cells with concemitant release of undesirable biological materials such as cytochromes, pigments, enzymes, chemicals and other undesirable cellular constituents and debris, is prevented. Large scale recovery and purification of proteins is greater than that obtained from prior art methods. Active Angiostatin can be stored in buffers for extended periods of time, in vials or other containers, either in solution which may be Human; plasminogen; angiostatin; greenstatin; thrombolytic factor; angiogenesis inhibitory protein; proliferation; angiogenesis; cancer; Amino acid seguence of human greenstatin protein. AAY53869 standard; protein; 254 AA. 13-MAR-2000 (first entry)

vascular endothelial cell; ophthalmic disease; glaucoma; diabetic retinopathy; arthritis; psoriasis.

Homo sapiens.

anion a

W09961464-A1

Hong Lee JH, Purifying angiogenesis inhibitors produced as recombinant proteins in Escherichia coli, useful as anticancer agents and for treating ocular

The present sequence represents the human greenstatin protein. It is derived from the plasminogen protien, and comprises amino acids 101-354. Angiostatin is also derived from plasminogen, and comprises amino acids 99-467. Angiostatin and greenstatin are used as amino acids 99-467. Angiostatin and greenstatin are used as thrombolytic factors and angiogenesis inhibitory proteins. Angiostatin contains the kringle 1-4 region of plasminogen, and greenstatin contains the kringle 1-3 region of plasminogen. As both proteins contains the kringle i-3 region of plasminogen. As both proteins contain a high specification describes a method for the purification of such angiogenesis inhibitory proteins. The method comprises solubilising the proteins, produced as inclusion bodies in Eschericina coll and refolding the solubilised fraction in buffer containing urea and glutathione. The angiogenesis inhibitory proteins specifically inhibit proliferation of vascular endothelial cells, but not that of non-endothelial cancers or normal cells. The angiogenesis inhibitory proteins are used to suppress angiogenesis, specifically for treating cancers (e.g. of lung, skin and brain) or ophthalmic diseases (e.g. glaucoma and diabetic retinopathy), but also arthritis and psoriasis.

245 126 NGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCFTT 185 148 305 66 PWCYIIDPCVRWEYCNLIQCSEIESGVLEIPTVVPVPSMEAHSEAAPTEQTPVVRQCYHG 125 149 DPNKRWELCDIPRCT-----TPP-----PSSGPTYO--CLKCTGENYRGNVAVTVSGH 194 61 7 DCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ-DPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGT PCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC Indels 50; Gaps Length 254; 62 PWCYTTDPEKRYDYCDILECEE------

AAY53869

X H X H X Z Z

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The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of anglostatin fragment, or combination of anglostatin fragments, or aggregate angiostatin The fragment is preferably derived from murine, name, thesus, porcine or bovine plasminogen and is a kringle 1.6 kringle 2, kringle 3, kringle 2.3 kringle 1.3 kringle 1.2 kringle 1.4 or kringle 1.4 kringle 1.4 kringle 1.4 kringle 1.4 kringle 1.5 kringle 1.5 kringle 1.5 kringle 1.5 kringle 1.5 kringle 1.5 kringle 1.6 for 5 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating and suglogenesis-madiated dispasses such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

C The present sequence, Rhesus kringle 1.3, is a specific angiostatin fragment which can be used in the invention, and represents amino caids 6-255 of Rhesus angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.4%; Score 704; DB 17; Length 250; Best Local Similarity 42.5%; Pred. No. 5.1e-38; Matches 127; Conservative 40; Mismatches 82; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cao Y, Folkman MJ, Lin J, Oreilly MS, Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 125-126; 203pp; English
                                                                                                                                                                                                     AAW07568 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0612788.
95US-0429743.
96US-0605598.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus kringle 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA;
253 DS 254
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26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                22-JUN-1997
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                                                                                                                                                                                                                                                                                   AAW07568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesus.
                                                                                                                    RESULT 15
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67 WCYTYDDCVRWEYCNLJQCSETESGVLETPTVVPVPSNEAHSEAAPTEQTPVVRQCYHGN 126

61 WCYTTDPEERFDYCDIPECED-------

127 GOSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDADIGPWCFITD 186

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187 PSIRWEYCNLFRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKAFTVTGTP 246
                                                                                         247 CQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYIWNPRKLFDYCDIPLC 305
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STREET: 111 PERGILLEE SITEEL, 3/IN FLOOT
CITY: Atlanta
STATE: Georgia
COUMTR: A. 15.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PATCHILD Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FLING DATE:
CLASSIFICATION: 514
ATCREEY AGENT INFORMATION:
NAME: WEATCH NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANE: 404-818-3790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID 30.00
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bovine; IMMEDIATE SOURCE: CLONE: K1-3
US-08-612-788-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                               US-08-612-788-33
RESULT 1
 September 29, 2003, 08:01:08; Search time 29 Seconds (without alignments) 449.370 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32,
Sequence 31,
Sequence 31,
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                                                                                                                                                                                                      1 KSPVVQDCYHGDGRSYRGIS.......YIMNPRKLFDYCDIPLCASS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32,
Sequence 32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3 Sequence 3 Sequence 3 Sequence 3 Sequence 2 
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Sequence 2
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Parge_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Parge_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                       US-10-088-548-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                        Perfect score:
Sequence:
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                                                                            OM protein
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                                                                                                            Run on:
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No.
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Sequence
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Sequence
                                                                                                                      Sequence 33, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Folkman, M. Applicant: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
ALIGNMENTS
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ATTOREST AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEFRONE: 404-818-3700
TELEFRAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                        Best_Local Similarity 42.19
Matches 126; Conservative
      ; ORGANISM: Bovin
; IMMEDIATE SOURCE:
; CLONE: K1-3
US-09-066-028-33
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                                                                                          Query Match
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                                                                                                                                      67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                      187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                         61 WCYTTDPDKRYDYCDIPECED------KCMHCS 87
                                                                     8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ-P 66
                                                                                                                                                                                                                                                                                                                                                        247 COEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                         50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FOLKMEN, M. Judah
APPLICANT: PO'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sao, Yihai
APPLICANT: Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
WOMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
     Length 250;
                                      80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE PORM:
MEDITUR TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
   Query Match 40.1%; Score 716; DB 2; Best Local Similarity 42.1%; Pred. No. 1.8e-57; Matches 126; Conservative 43; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/09066028 Patent No. 6024688 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 250 amino acids TYPE: amino acid STRANDEDNESS:
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Query Match
Best Local Similarity
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STATE: Georgia
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ORIGINAL SOURCE:
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ANTI-SENSE: N
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67 WCYTTDDCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::| | : |::|| ||:|| ||:|| | :|| | ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WCYTTDPDKRYDYCDIPECED------KCMHCS 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CYHGDGRSYRGISSTIVTGRTCQSWSSMIPHWHQRIPENYPNAGLTENYCRNPDSGKQ-P
                                                                                                                                                      Gaps
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Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Rallly, Micheal
Cac, Yilhai, B. Kim Lee
ITTLE OF INVENTION: Andjostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE: 10303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIN RELEASE #1.0, Version #1.30
CURRINT APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION OF COMPANIAN APPLICATION 1099
40.1%; Score 716; DB 3; Length 250;
42.1%; Pred. No. 1.8e-57;
Live 43; Mismatches 80; Indels
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STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
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127 GOSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDADIGPWCFIID 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 GEHYEGKISKTMSGIECQSWGSQSPHAHGYLPSKFPNKNLKANYCRNPDGEPRPWCFTTD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 CQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                     8 CYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRIPENYPNAGLTENYCRNPDSG-KQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                   40.0%; Score 715; DB 2;
11arity 42.5%; Pred. No. 2.2e-57;
Conservative 41; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTATION NUMBER: 36,714
REFERENCE/DOOKET WUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09/066,028
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Patent No. 6024688
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PAtentin Release #
                                                                                                                                      N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & A
                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: N-tern
ORIGINAL SOURCE:
ORGANISM: POICINE
      amino acid
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 127; Conserva
                                                  linear
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CLASSIFICATION:
                                                                                                                                                                                               ; IMMEDIATE SOURCE:
; CLONE: K1-3
US-08-612-788-32
                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-066-028-32
                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 POKRWEFCDIPRCT ---- TPP --- - PSSGP -- KYQCLKGTGKNYGGTVAVTESGHT 193
                                                                                                                                                                                                                                                                                                                              8 CYHGDGRSYRGISSTTVIGRICQSWSSMIPHWHQRIPENYPNAGLTENYCRNPDSGKQ-P 66
                                                                                                                                                                                                                                                                                                                                                       247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sin, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
CORRESPONDENCE: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          40.1%; Score 716; DB 4; Length 250; 42.1%; Pred. No. 1.8e-57;
                                                                                                                                                                                                                                                                                     80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Georgia
COUNTRY: U.S.
ZIP: 3303-1763
ZIP: 3303-176
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                     43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew
STRER: 191 Peachtree Street, 37th Floor
CITY: Allanta
STATE: Georgia
                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,714
36,714
36,716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 0521
TELECOMMUNICATION INFORMATION:
TELEFRAX: 404-818-3700
TELEFRAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 250 amino acids
                                                                                                             ORGANISM: Bovine IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                            Best Local Similarity 42.19
Matches 126; Conservative
                         HYPOTHETICAL: NO
                                                                                                                                                      CLONE: K1-3
                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                               8-09-335-325-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-612-788-32
                                                                                                                                                                                                                                            Query Match
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us-10-088-548-2.sep29.rai

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Query Match 40.0%; Score 715; DB 4; Best Local Similarity 42.5%; Pred. No. 2.2e-57; Matches 127; Conservative 41; Mismatches 81.
                    NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REGISTRATION NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acid
STRANDENRES: CUDKNOWN>
OULENOTH: 11near
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 191 Peachtree Street, 37th Floor CIY: Atlanta STATE: Geordia
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 32:
        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Porcine IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                    CLONE: K1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
ZIP: 30303-1769
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US-08-612-788-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 WCYTTDPETREDYCDIPECED------ECMHCS 87
                                                                                                                                                                                                                                                                                                                                                                                                                        8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSG-KQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 CQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
O'Stilly, Micheal
Co'N Yiha Lee
Sin, B. Kin Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                                                                                                                                            Query Match 40.0%; Score 715; DB 3; Length 250; Best Local Similarity 42.5%; Pred. No. 2.2e-57; Matches 127; Conservative 41; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <ur>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IEM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
LELEFAX: 404-818-3709
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHRRACTERICS:
LENGTH: 250 amino acid
STRANDEDNESS:
TOPOLOGY
                                                                                                                                                                                                                  N-terminal
                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                        Porcine
                                                                                                                                                                                                                FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: K1-3
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S-09-335-325-32
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67 WCYTTDPCVRWEYCNLFQCSETESGVLETPTVVPVPSNEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 PNKRWEFCDIPRCT-----TPP-----PTSGPTYQ--CLKGRGENYRGTVSVTASGHT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 GEHYBGKISKIMSGIECQSWGSQSPHAHGYLPSKFPNKNLKMNYCRNPDGEPRPWCFTTD 147
                                                                                                                                                                              1 CKIGNGKNYRGTISKIKSGVICQKWSVSSPHIPKYSPEKFPLAGLEENYCRNPDNDEKGP 60
                                                                                                                                      8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSG-KQP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08612788
Patent No. 5875682
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Co'Reilly, Micheal
APPLICANT: Co', Yihai
APPLICANT: So', Yihai
APPLICANT: So', Yihai
APPLICANT: Si'm B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
Length 250;
                                                                 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 GENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDGEPRPWCFTTD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQSYRGIFSTTVIGRICQSWSSMIPHRHQRIPENYPNDGLTMNYCRNPDADIGPWCFIID 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CKTGNGKNYKGTMSKTRTGITCQKWSSTSPHRPTFSPATHPSEGLEENYCRNPDNDGQGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDS-GKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cao, Yihai Sim, B. Kim Lee Sim, B. Kim Lee Sim, B. Kim Lee NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82; Indels
  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.4%; Score 704; DB 3;
42.5%; Pred. No. 2.2e-56;
tive 40; Mismatches 82;
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61 WCYTTDPEERFDYCDIPECED--------
                                                                                                                                                                                                                                   05213-0126
                                           APPLICATION NUMBER: US/09/066,028 FILING DATE:
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/0933535
Patent No. 6521439
GENERAL INFORMATION:
RAPLICANT: Folkman, M. Judah
                                                                                                                                                                                      NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERRNCE/POCKET NUMBER: 0521;
TELECOMMUNICATION INFORMATION:
TELEPRONE: 404-818-3709
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Reilly, Micheal
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rhesus monkey IMMEDIATE SOURCE: CLONE: K1-3
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 250 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.59
Matches 127; Conservative
                           URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                FILING DATE:
      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-066-028-31
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US-09-335-325-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDS-GKQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09066028
Patent No. GO24688
GENERAL INFORMATION:
APPLICANT: Pollman, M. Judah
APPLICANT: Cao, Willy, Micheal
APPLICANT: Cao, Willy Micheal
APPLICANT: Sao, Will Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF EQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

39.4%; Score 704; DB 2;
Best Local Similarity 42.5%; Pred. No. 2.2e-56;
Matches 127; Conservative 40; Mismatches 82
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191 Peachtree Street, 37th Floor
                                                       ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION WUMBER: 95,714
REFERENCE/DOCKET WUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE GHARACTERISFICS:
LENGTH: 250 amino acids
TTPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 WCYTTDPEERFDYCDIPECED-----
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z1F: 2000 100 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rhesus monkey
IMMEDIATE SOURCE:
CLONE: K1-3
                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                      TYYE.
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                        CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 191 Per CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgia
                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: NORIGINAL SOURCE:
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US-09-066-028-31
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SSEE: Jones & Askew
P: 191 Peachtree Street, 37th Floor
Atlanta
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEPRA: 404-818-3799
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/09066028; Patent No. 6024688; GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Cao, Yihai, APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 250 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: KI-3
US-08-612-788-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
              CORRESPONDENCE ADDRESS:
                                                                         STATE: GEC.
COUNTRY: U.S.
30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                     FILING DATE:
                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-066-028-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŽ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 WCYTIDPCVRWEYCNLIQCSEIESGVLEIPTVVPVPSMEAHSEAAPTEQIPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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APPLICANT: FOlkman, M. Judah
APPLICANT: Co. Yihai
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
COMPUTER READABLE FORM:

MEDIUM TIPE: RIOPPY disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRAPE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 17-Dun-1999
CLASSIFICATION NUMBER: US/09/335,325
FILING DATE: 17-Dun-1999
CLASSIFICATION NUMBER: US/08/612,788
FILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/08/612,788
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/08/612,788
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 35,74
REGISTRATION NUMBER: 35,74
REFERENCE/DOCKET NUMBER: 05213-0126
FILINGTRATION INCRMATION:
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE: CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: CUNKNOWN>
MOLECULE TYPE: protein
HYPOTHERICAL: NO
ANTT-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.4%; Score 704; DB 4; Length 250; Best Local Similarity 42.5%; Pred. No. 2.2e-56; Matches 127; Conservative 40; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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US-00-612-788-30
Sequence 30, Application US/08612788
Patent No. 5837682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rhesus monkey IMMEDIATE SOURCE:
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88 GENYDGKISKTMSGLECQAWDSQSPHAHGXIPSKFPNKNLKKNYCRNPDKELRPWCFTTD 147
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|- ----TPP-----PSSGPIYQ--CLKGTGENYRGNVAVTVSGHT 193
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39.4%; Score 703; DB 2; Length 250;
Best Local Similarity 42.5%; Pred. No. 2.7e-56;
Matches 127; Conservative 39; Mismatches 83; Indels
ZIE: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PASTENTIN PRELABS # 1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
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GENERAL INFORMATION:
APPLICANT: FOLKMan, M. Judah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                              STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQ-P
  FITLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.4%; Score 703; DB 3; Length 250;
ilarity 42.5%; Pred. No. 2.7e-56;
Conservative 39; Mismatches 83; Indels
                                                                                                                                                  ZUP: 30303-1769
ZUP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PETCATLON PC-DOS/MS-DOS
SOFTMARE: PETCATLON DATA:
APPLICATION NUMBER: US/09/066,028
                                                          ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/COCKET NUMBER: 05213-0126
TELECOMMUNICATION INPORMATION:
TELEPHONE: 404-818-3799
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: .404-818-3799
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OKGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                        Georgia
                                                                                                  Atlanta
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US-09-335-325-30
                                                                                                                  STATE: GE
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Matches 127;
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; Sequence 30, Application US/09335325 ; Patent No. 6521439

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67 WCYTIDPCVRWEYCNLIQCSETESGVLEIPTVVPVPSMEAHSEAAPIEQIPVVRQCYHGN 126
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Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 250;
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                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PACHATIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                                                                                                                                        ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 703; DB 4;
42.5%; Pred. No. 2.7e-56;
live 39; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: 30: US-09-335-325-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-Jun-1999 CLASSIFICATION: 
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 250 amino acids TYPE: amino acid STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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INFORMATION FOR SEQ ID NO: 30:
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67 WCYTTDPCVRMEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- BCMICS 87
Query Match 39.2%; Score 700; DB 3; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: CO'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          CITE.: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05213-0126
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATORNEY-AGENY INFORMATION:
NAME: WARTEN, WIlliam L.
REGISTRATION NUMBER: 36,714
REPERSORMUNICATION INFORMATION:
TELEDEDONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WCYTTDPDKRYDYCNIPECEE----
                                                                            RESULT 14
US-00-066-028-29
: Sequence 29, Application US/09066028
; Patent No. 6024688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 250 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Murine IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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US-09-066-028-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                  Sequence 29, Application US/08612788
Patent No. 5837682
GENERAL INCRMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Cao, Xihai
APPLICANT: Cao, Xihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Application Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.2%; Score 700; DB 2; Length 250;
41.1%; Pred. No. 5e-56;
Live 37; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: RAPLICATION NOMBER: US/08/612,788 TLING DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                    E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGIETRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3709
TELEPHONE: 404-818-3799
                                                                                                                                                                                                                                                                                                                                        COUNTRY U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
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amino acid
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Best Local Similarity 41.15
Matches 123; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: K1-3
                                                                                                                                                                                                                                                                                                                             Georgia
                                                                                                                                                                                                                                                                                                         CITY: Atlanta
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                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-612-788-29
                                       RESULT 13
US-08-612-788-29
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SETT 15	Qy fa	COEWAAOEPHRESTEIDGINKWAGLEKNYCRNPOGDINGPWCYTMNPRKLEDYCDIPLC	qq	
Content to Con	E	134 CQKWSEQIPHKHNK-TPENFPCKNLEENYCRNPDGE-TAPMCYTTDSQLRWEYCEIPSC	Qy Db	
### APPLICANT POLITY, Michael CONTINGENOUS MANAGEMENTS AND ADDRESS OF THAT AD	Sequenc ; Sequenc ; Patent	325-29 = 29, Application US/09335325 transparence:	Q _Y Db	247 CQEWAAQEPHRHSTFI : : 194 CQRWSEQTPHRHNR-T
TITLE OF INTERVALLE AND LEER TOTAL PROGRESS AS A		APPLICANT: Folkman, M. Judah O'Reilly, Micheal Cao, Yihai	Search Job tim	completed: September 29 ne : 30 secs
ADDRESSEE: Jones & Askew STREET: 1919 Peachtree Street, 37th Floor CITY: Atlanta CONTYER COCYTA CONTYER: 0.53 COMMINE: 10.5 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EMPERITOR DATA: COMPUTER: PATENTON NUMBER: US/09/135,325 FILING DATE: 17-3nn-1999 CLASSITICATION DATE: TO-NUMBER: US/09/135,325 FILING DATE: CONKOWND- ATDENTY APPLICATION NUMBER: US/09/135,325 FILING DATE: CONKOWND- ATDENTY AREA OF THE PROMATION: APPLICATION NUMBER: US/09/012,788 FILING DATE: CONKOWND- ATDENTY ACRIA HISPORMATION: TELEBROWE: CAPACTER TIPES AND TELEBROME: 404-818-3700 TELEBROWE: CAPACTER TIPES AND TELEBROME: 404-818-3700 TELEBROWE: CAPACTER TIPES: AND CAPACTER TYPE: AND CAPACTER TYPE: AND CAPACTER TYPE: AND CAPACTER TYPE: DOTO-TO-TO-TO-TO-TO-TO-TO-TO-TO-TO-TO-TO-		SlE, B. Kim Lee FITLE OF INVENTION: Angiostatin Fragments and Method of Use WOMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:		
COMPUTER: U.S. COMPUTER: TOWN COMPUTER: TEAL ALL GOOD distance of the comparation of th				
COMPUTER: READABLE FORN: MUDIOM TYPE: FLOPPY disk COMPUTER: LIDEPY disk COMPUTER: LIDEP COMPATA: SOFTWARE: RATEORITON NOTA: APPLICATION NOMBER: US/09/335,325 FILING DATE: COMPATO: APPLICATION NOMBER: US/09/612,788 FILING DATE: COMPATO: TELEPHONE: CHARACTERISTICS: AND TELEPHONE: CHARACTERISTICS: AND TOPOLOGY: Linear MOLECULE TYPE: Drotein HYPOTHERICAL: NO ANTI-SENSE: NO CREANISH: MATINE COLONE: XI-3 SEQUENCE COLONE: AI-18; Pred. NO: 29: ORGANISH: WAITHE CLONE: XI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: BEST LOCAL SIMILATITY 41.18; Pred. NO CLONE: XI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: ABSCRIPTION: XI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: CLONE: XI-3 SEQUENCE SIMILATITY 41.18; PRED. NO: 29: 1		C111: ALLanca STATE: Georgia COUNTRY: U.S.		
MEDIUM TYPE: Floppy disk COMPUTER: We PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAPLICATION DATA: APPLICATION NOMER: US-09/9335,325 FILING DATE: U1-Jun-1999 PRIOR APPLICATION NUMBER: US/08/612,788 TILING DATE: U1-Jun-1999 CLASSIFICATION NUMBER: US/08/612,788 TILING DATE: U1-Jun-1999 CLASSIFICATION NUMBER: US/08/612,788 TILING DATE: U1-Jun-1999 TREEDRACE/DOCKET UNMBER: S3,714 REFERENCE/DOCKET UNMBER: S3,714 REFERENCE/DOCKET UNMBER: S3,714 REFERENCE/DOCKET UNMBER: S2,100 TELEPAX: 404-818-3790 INFORMATION FOR EQ. DIO NO: 29: SEQUENCE CHARACTERISTICS: LENGTH: 250 amino acids TYPE: amino acids TYPE: Brotein HUMBIALE SOURCE: ORGENIEM: Note and acids TYPE: ROUTE: Under and acids TYPE: N-terminal ORIGINAL SOURCE: ORGENIEM: Wutnine IMMEDIATE SOURCE: CRANKER: Multine IMMEDIATE SOURCE: CRANKER: MATCH 39.28; SCOTE 700; DB 4; Length 250; MATCHES 123; CONSETVATION: SEQ ID NO: 29: 1		ZIP: 30303-1769 COMPUTER READABLE FORM:		
CURRENT APPLICATION NUMBER: 105,09/335,325 CURRENT APPLICATION NUMBER: 105,09/335,325 FILING DATE: 17-Jun-1399 CLASSIPICATION NUMBER: 05/09/335,325 FILING DATE: 17-Jun-1399 CLASSIPICATION NUMBER: 05/08/612,788 FILING DATE: 07-1399 CLASSIPICATION NUMBER: 05/14 REPERENCE/DOCKET NUMBER: 05/14 REPERONE: 10-18-3799 INFORMATION FOR SEQ ID NO: 29: SEQUENCE TRANSCTERISTICS: LENGTH: 250 amino acids TELECOMMUNICATION NO: 29: SEQUENCE TRANSCTERISTICS: LENGTH: 250 amino acids TYPE: amino acids TYPE: ADDITION OCIDS: 11-10-10-10-10-10-10-10-10-10-10-10-10-1		MEDIUM TYPE: Floppy disk COMPUTER: IBM PC comparatible		
APPLICATION NOBER: US/09/335,325 FILING DATE: T0-2m1-1999 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/612,788 FILING DATE: CURKNOWN- ATORNEY/AGENT INFORMATION: NAME: Warren, William L. REGESTRATION NUMBER: 05,714 REFREENCE/DOCKET NUMBER: 05,714 REFREENCE/DOCKET NUMBER: 05,714 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OCCIDENCE: CONTROL OCCIDENCE CHARACTERISTICS: LENGTH: 250 amino acid STRANDEDNESS: CURNOWN- TYPE: amino acid STRANDEDNESS: CURNOWN- TYPE: MOLECULE TYPE: Protein HYPOPHETICAL: NOLECULE TYPE: Protein HYPOPHETICAL: ORGANISM: Murine CLONE: KI-3 SEQUENCE: DESCRIPTION: SEQ ID NO: 29: ONERTY MATCH MATCHER SOURCE: ORGANISM: Murine LONGENCE: DESCRIPTION: SEQ ID NO: 29: ONERTY MATCH Best Local Similarity 41.1%; Pred. NO. 5e-56; MATCHER SOURCE: MATCHER SOURCE: ORGANISM: MATCH RECORDER SOURCE: ORGANISM: MATCH RECORDER SOURCE: ORGANISM: MATCH RECORDER SOURCE: ORGANISM: MATCH SOURCE: ORGANISM: MATCH STREAMSTRESOVACQUE SUPPRIVEDER NUMBER DEB		OFERFILMS SISTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30		
PRIOR CARSAFICATION DATA: CHASSIFICATION DATA: APPLICATION DATE: APPLICATION NUMBER: US/08/612,788 ATTUND DATE: ATTUND DATE		PAPELICATION NOMBER: 0S/09/335,325 FILING DATE: 17-Jun-1999		
ATTORNEY/AGENT INFORMATION: MARBE: Wattern, William L. REGISTRATION NUMBER: 36,714 REFERENCE/DOCKET NUMBER: 36,714 REFERENCE/DOCKET NUMBER: 36,714 REFIERDNICATION INFORMATION: TELEPRAX: 404-818-3790 INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS: LENGTH: 250 amino acids STRANDEDNESS: (GTKNOWN) TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHERICAL: NO REGISTRANDEDNESS: (GTKNOWN) TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHERICAL: NO REGISTRANDEDNESS: (GTKNOWN) TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHERICAL: NO REGISTRANDEDNESS: (GTKNOWN) ORGANISM: Murine IMMEDIATE SOURCE: CLONE: K1-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: CLONE: K1-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: ASS-325-29 OUBLY MATCH 39.2%: SCOIE 700; DB 4; Length 250; Matches 123; CONSETVATION: MISMATCHES 89; Indels 50; Gaps REGISTRATICE SOURCE: (LI		CLASSIFICATION: <unknown> PRIOR APPLICATION DATA:</unknown>		
ATTORNATION: NAME: Watten, William L. REGISTRATION NUMBER: 36,714 REGISTRATION NUMBER: 05213-0126 TELEPAX: 404-818-3700 TELEPAX: 404-818-3700 TELEPAX: 404-818-3700 INFORMATION FOR SEQ 1D NO: 29: SEQUENCE CHARACTERICS: LENGTH: 250 amino acids TYPE: amino acid TYPE: mino acid TYPE: protein HYPOTHERICAL: NO ANTI-ENENSE: NO GRGANISM: Murine IMMEDIARE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ 1D NO: 29: SEQUENCE DESCRIPTION: SEQ 1D NO: 29: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ 1D NO: 29: SEQUENCE DESCRIPTION: SEQ 1D NO: 29: GLONE: XI-3 SEQUENCE DESCRIPTION: SEQ 1D NO: 29: AMACHES 123; CONSETVATION: SEQ 1D NO: 5e-56; MATCHES 123; CONSETVATION: SEQ 1D NO: 29: REGINAL SURVERIES SOURCE: CLONE: XI-3 SEQUENCE DESCRIPTION: SEQ 1D NO: 29: SEQUENCE DESCRIPTION: SEQ 1D NO: 29: AMACHES 123; CONSETVATION: SEQ 1D NO: 6e-56; MATCHES 123; CONSETVATION: SEQ 1D NO: 6-56; MATCHES 123; CONSETVATION: SEQ 1D NO: 19: 1 1 1 1 1 1 1 1 1 1 1 1 1		APPLICATION NUMBER: US/08/612,788 FILING DATE: <unknown></unknown>		
REPERENCE NUMBER: 05.13-0126 TREDEPHONE: 404-818-3700 TRELEPHONE: 404-818-3700 TOPOGOGN: 110-818-3700 TOPOGOGN: 110-818-3700 TOPOGOGN: 404-818-3700 TREAGNEST TYPE: NO REAGNEST TYPE: NO REAGNEST TYPE: NO REAGNEST TYPE: NO REAGNEST TYPE: 1118-370 TOPOGOGN: 41.18-370 TRELEPHONE: 41.18-370 TOPOGOGN: 4		NATORNEY/AGENT INFORMATION: NAME: WAITEN I.		
TELEPHONE: 404-818-3700 TELEPAX: 404-818-3799 INFORMATION FOR EQO ID No. 29: SEQUENCE CHARACTERISTICS: LENGTH: 520 annino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO CREANISM: Murine HYPOTHETICAL: NO ANTI-SENSE: NO CREANISM: Murine IMMEDIATE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: Autch IMMEDIATE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: Autch IMMEDIATE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: Autch IMMEDIATE SOURCE: IMMEDIATE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: Autch IMMEDIATE SOURCE: IMMEDIATE SOURCE: CLONE: KI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: IMMEDIATE SOURCE: IMMEDIATE		REGIZIATION NUMBER: 98 / 14 REFERENCE/DOCKET NUMBER: 05213-0126 FELECOMMUNICATION INPORMATION:		
INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS: LENGTH: 250 anino acids TYPE: amino acids TYPE:	•• ••	TELEPHONE: 404-818-3700 TELEPAX: 404-818-3799		
LENGTH: 250 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acid TYPE: amino a	INFOR	MATION FOR SEQ ID NO: 29:		
STRANDEDNESS: <pre></pre>		LENGTH: 250 amino acids TYPR: amino acids		
MOLECULE TYPE: protein HYPOTHERICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Murine INMEDIATE SOURCE: CLONE: K1-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: -09-335-325-29 39.2%: Score 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 8 CYHGDGRSYRGISSTYUTGTOSWRSHIPHWPRTPENYPNAGLTENYCRNEDSGRQ-P		STRANDENNESS (Thrown>		
PROTI-SENSE: NO PRAGRISM: N. Letrninal ORIGINAL SOURCE: ORGANISM: Murine IMMEDIATE SOURCE: CLONE: K1-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: SEQUENCE DESCRIPTION: SEQ ID NO: 29: Ouery Match 39.2%; Score 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps RICHGDGRSYRGISSTTYTGRTCOSWSSMIPHWHORTPENYPNAGLIENYCRNPDSGRQ-P 66 CYNGIGNSTROTHERSTANDENCRNPDNDEGGF 60 OF WCYTTDPCVRWEYCHIPHOCSFESSOLEFPTVPVRYSPTHPNEGLENYCRNPDNDEGGF 60 HILLI		MOLECULE TYPE: protein		
ORIGINAL SOURCE: ORGANISM Murine IMMEDIATE SOURCE: CLONE: XI-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: 109-335-325-29 SECTED SECTION: SEQ ID NO: 29: 39.2%; SCORE 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 8 CYHGDGRSYRGISSTYUTGCNEWRIPHWHORTPENYPNAGLTENYCRNEDSGRQ-P 66		NATI-SENSE: NO PRAGMENT TYPE: N-terminal		
IMMEDIATE SOURCE: CLONE: K1-3 SEQUENCE DESCRIPTION: SEQ ID NO: 29: SEQUENCE DESCRIPTION: SEQ ID NO: 29: Ouery Match 39.2%; Score 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 8 CYHGDGRSYRGISSTTVTGRTCOSWSMIPHWHORTPRNYPNAGLTENYCRNDSGRO-P 66		ORIGINAL SOURCE:		
SEQUENCE DESCRIPTION: SEQ ID NO: 29: -09-335-325-29 Subery Match 39.2%; Score 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps R CYHGDGRSYRGISSTTVTGRTCOSWSSMIPHWHORTPENYPNAGLIENYCRNPDSGRQ-P 66 R CYHGDGRSYRGIMSTRKSGVAGWWGATFFHVPNYSPSTHPNEGLENYCRNPDNDEGGP 60 WCYTTDPCVRWBYCNITGCSFTESGVLETPTVVPVPSNEAHSEAAPTBQTPVVRQCYHGN 12		IMMEDIALSH: MULIHE IMMEDIALS STARTS CHARE X1-X CHARE X1-X		
Duery Match 39.2%; Score 700; DB 4; Length 250; Best Local Similarity 41.1%; Pred. No. 5e-56; Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWPRTPENYPHAGLTENYCRNPDSGRQ-P 66	; US-09-335	ID NO:		
Matches 123; Conservative 37; Mismatches 89; Indels 50; Gaps 8 CYHGDGRYRGISSTTVTGRTCOSWSSHTHWHORTPENYPNAGLTENYCRNPDSGKQ-P 66 1	Query M Best Lo	39,2%; Score 700; DB 4;		
8 1 67	Matches	Conservative 37; Mismatches 89; Indels 50; Gaps		
1 67	QY	CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQ-P		
63	셤	CKTGIGNGYRGTMSRIKSGVACQKWGAIFPHVPNYSPSTHPNEGLEENYCRNPDNDEQGP		
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September 29, 2003, 08:03:07; Search time 347 Seconds (without alignments) 134.301 Million cell updates/sec
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1786
1 KSPVVQDCYHGDGRSYRGIS......YTMNPRKLEDYCDIPLCASS 308
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(cgn2_6/ptodata/1/pubpaa/0008_NEW_PUB.ppp:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566894 seqs, 151307093 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
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                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 308
                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 33, Appl Sequence 33, Appl	Sequence 33, Appl Sequence 32, Appl	Sequence 32, Appl	Sequence 32, Appl Sequence 61, Appl	Sequence 31, Appl	Sequence 31, Appl Sequence 31, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 30, Appl	Sequence 29, Appl	Sequence 29, Appl
SUMMARIES	US-09-761-120-33 US-09-335-325-33	US-10-131-241-33 US-09-761-120-32	US-09-335-325-32	US-10-131-241-32 US-10-131-241-61	US-09-761-120-31	US-09-335-325-31 US-10-131-241-31	US-09-761-120-30	US-09-335-325-30	US-10-131-241-30	US-09-761-120-29	US-09-335-325-29
% Query Match Length DB	250 9	250 15 250 9	250 10	250 IS	250 9	250 10 250 15	250 9	250 10	250 15	250 9	250 10
% Query Match 1	40.1	40.1	40.0	40.0 39.8	39.4	39.4 39.4	39.4	39.4	39.4	39.5	39.5
Score	716	716	715	711	704	704 704	703	703	703	700	700
Result No.	170	m 4	ស	7 0	80 (204	11	12	13	14	15

Sequence 29, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 1, Appl	Sequence 26, Appl Sequence 26, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl	Sequence 38, Appl Sequence 37, Appl Sequence 37, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl
# 10 0 0 # 0 0 # m	0 0S-09-761-12 0 0S-09-335-3 0 0S-09-761-12 0 0S-09-761-12 0 0S-09-761-12 0 0S-09-35-3 0 0S-09-35-3 0 0S-09-35-3 0 0S-09-35-3 0 0S-09-35-3 0 0S-09-335-3	15 US-10-111-241-38 9 US-09-76-120-37 10 US-09-335-325-37 11 US-10-131-241-37 9 US-09-76-120-36 10 US-09-335-325-36 15 US-10-131-241-36 9 US-09-761-120-35 10 US-09-335-325-35 15 US-10-131-241-35 15 US-10-131-241-35
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ALIGNMENTS

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Sequence 33, Application US/09761120

Sequence 33, Application US/09761120

Patent No. US20020037847A1

GENERAL INFORMATION:

APPLICANT: FOLKman, M. Judah

APPLICANT: POLKman, M. Judah

APPLICANT: POLKMAN, Nachael

TITLE OF INVENTION: Nachael

CURRENT PELICATION NUMBER: US/09/761,120

CURRENT APPLICATION NUMBER: 09/309,821

PRIOR FILING DATE: 1999-05-11

PRIOR FILING DATE: 1999-05-11

PRIOR FILING DATE: 1999-05-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0

LENGTH: 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.1%; Score 716; DB 9; Length 250; Best Local Similarity 42.1%; Pred. No. 7.7e-55; Matches 126; Conservative 43; Mismatches 80; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; OTHER INFORMATION: Kringle 1-3 US-09-761-120-33
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bos sp. FEATURE:
US-09-761-120-33
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Wed Oct

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APPLICANT: BOldady, John W.
APPLICANT: Boldady, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell ProlifITILE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers FILE REPERENCE: 05213-0344 43170-271565
CURRENT APPLICANTON NUMBER: US/10/131,241
CURRENT APPLICANTON NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 GOSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLTMNYCRNPDADIGPWCFIID 186
                                                                                                                                                                                                                             187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                        67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 PQKRWEFCDIPRCT-----TPP-----PSSGP--KYQCLKGTGKNYGGTVAVTESGHT 193
                                                67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
                                                                                                                                      127 GOSYRGTFSTIVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADTGPWCFITD 186
                                                                                                                                                              1 CKTGNGQTYRGTTAEIKSGYTCQKWSAISPHVPKFSPEKFPLAGLEENYCRNPDNDENGP 60
                                                                                                                                                                                                                                                                                                                   247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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40.1%; Score 716; DB 15; Length 25(
Best Local Similarity 42.1%; Pred. No. 7.7e-55;
Matches 126; Conservative 43; Mismatches 80; Indels
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US-09-761-120-32
; Sequence 32, Application US/09761120
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; Sequence 33, Application US/10131241
; Publication to US20030012792A1
; ENERAL INFORMATION:
                                                                                          61 WCYTYDPDKRYDYCDIPECED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Bovine
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                                                                                          PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                    GOSTRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDADIGPWCFITD 186
                                              88 GENYEGKIAKTMSGRDCQAWDSQSPHAHGYIPSKFPNKNIKMNYCRNPDGEPRPWCFTTD 147
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                                                                                                                                                                                                        CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ-P
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Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: FOLMan, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INFORTION: Anglostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: IT-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: «UNKNOWN»
FILING DATE: «UNKNOWN»
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.1%; Score 716; DB 10;
42.1%; Pred. No. 7.7e-55;
iive 43; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren, William L.
REGISTRATION NUMER: 36,714
REGISTRATION NUMER: 36,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TXPE: FLOPPY GISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bovine IMMEDIATE SOURCE:
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 126; Conserv
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                                                                                          187
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APPLICANT: Holaday, John W.
APPLICANT: FOrtler, Anne H.
APPLICANT: Fortler, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell ProlifTILE OF INVENTION: Compositions and Regulating Anglogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US 102/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 715; DB 10; 42.5%; Pred. No. 9.4e-55;
                                                                                  FILING DATE: COLKNOWN)
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches
                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 32:
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/10131241 Publication No. US20030012792A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Porcine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 42.5% Matches 127; Conservative
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                  GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: O'Rellly, Michael
APPLICANT: O'Rellly, Michael
APPLICANT: O'Rellly, Michael
TITLE OF: INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
FILE REPERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: US/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
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Cao, Yihai
Sin, B. Kim Le
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.0%; Score 715; DB 9; Length 250;
42.5%; Pred. No. 9.4e-55;
Live 41; Mismatches 81; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
COURTNY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/0935325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Kringle 1-3
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Matches 127; Conservative
Patent No. US20020037847A1
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Sus sp.
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                                                                                                                                                                                                                                                                                                                   SEQ ID NO 32
LENGIH: 250
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Sequence 11. Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FOLKman W. Judah
APPLICANT: O'REALLY, Michael
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin
CURRENT APPLICATION NUMBER: 095040-011 (43171-252068)
CURRENT APPLICATION NUMBER: 09709/761,120
CURRENT FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR FILING DATE: 1997-05-30
                                                      244 GIPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIP 303
                                                                                                                                            196 GHTCQHWSAQTPHTHER-TPENFPCKNLDENYCRNPDGK-RAPWCHTTNSQVRWEYCKIP 253
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                            184 TIDPSIRWEYCNLFRCSDFEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVT 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 CQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09335325; Patent No. US20020164717A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 1-3
US-09-761-120-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 250
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                                                                                                                                                                                                                                                      258
                                                                                                                                                                                                       304 LCASS 308
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US-09-761-120-31
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US-09-335-325-31
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US-10-131-241-61

Sequence 61, Application US/10131241

Publication No. US20030012792A1

Sequence 61, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: FORTIGE.

TITLE OF INVENTION: and Regulating American decided for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating American US ing Cancer Markers

FILE REPRENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT PRILING DATE: 1099-10-06

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR PELLING DATE: 1999-05-21

PRIOR PELLING DATE: 1999-05-21

PRIOR PELLING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 65

SOFTWARKE: PatentIn Version 3.1
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                                                                                                                                                        40.0%; Score 715; DB 15;
42.5%; Pred. No. 9.4e-55;
tive 41; Mismatches 81;
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42.3%; Pred. No. 2.2e-54;
live 40; Mismatches 86;
SOFTWARE: Patentin version 3.1
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                                                                                         ORGANISM: Porcine
                                                                                                ; OKGANISH. F. C. US-10-131-241-32
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TYPE: PRT
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                                            LENGTH: 250
TYPE: PRT
                       SEQ ID NO 32
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Sequence 31, Application US/10131241
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Matches 127; Conservative
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ORGANISM: Rhesus monkey
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ORGANISM: Homo sapien
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US-09-761-120-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 PSIRWEYCNLTRCSDIEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CYHGDGRSYRGISSTTVIGRICQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDS-GKQP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 WCYTYDPEBREDYCDIPECED-----ECMHCS 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
Sim, B, Kim Lee TITLE OF INVENTION: Angiostatin Fragments and Method of Use NIWHER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.4%; Score 704; DB 10; Length 250; Best Local Similarity 42.5%; Pred. No. 8.6e-54; Matches, 127; Conservative 40; Mismatches 82; Indels 50;
                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.

ZIP: 30303-1769.

COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: II-Jun-1999
CLASSIFTCATION: <underware
CLASSIFTCATION: <underware
CLASSIFTCATION: <underware
CLASSIFTCATION: <underware
CLASSIFTCATION: <underware
COUNTRY
CLASSIFTCATION: <underware
CLASSIFT
                                                                                                                                                                ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORICATION NUMBER: US/08/612,788
FILIND DATE: CUDACON-
ATTORNEY/AGENT INFORMATION:
NUME: WARTER, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 250 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 404-818-3799 INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                       STATE: Georgia
                                                                                                                                                                                                                                        CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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ANTI-SENSE: NO
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RESULT 10 US-10-131-241-31

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Sequence 30, Application US/09761120

Sequence 30, Application US/09761120

Sequence 31, Application US/09761120

Setent No. US2002037847a1

SENERAL INFORMATION: M. Judah

APPLICAMT: Poliman, M. Judah

TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin

FILE REFERENCE: 05940-0151 (43171-252068)

CURRENT APPLICATION NUMBER: US/09/761,120

CURRENT APPLICATION NUMBER: 09/309,821

PRIOR FILING DATE: 1999-05-11

PRIOR FILING DATE: 1999-05-11

PRIOR FILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn Version 3.0

SEQ ID NO 30

LEMBTH: 250
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
JOHN W.
APPLICANT: Holdady, John W.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolif
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
GURRENT FILING DATE: 2002-07-22
FRIDE APPLICATION NUMBER: US 09/413,049
FRIOR PILING DATE: 1999-10-06
FRIOR PELING DATE: 1999-06-21
FRIOR PLING DATE: 1999-06-21
FRIOR APPLICATION NUMBER: US 60/086,586
FRIOR PLING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 31
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%; Score 704; DB 15;
42.5%; Pred. No. 8.6e-54;
iive 40; Mismatches 82;
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NAME/KEY: misc_feature
OTHER INFORWATION: Kringle 1-3
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FULLIARIENT FORTIER: Anne H.

APPLICANT: FOLICA: Anne H.

APPLICANT: FORTIER: Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proli

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proli

TITLE OF INVENTION: Composition and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR PLING DATE: 1999-05-21

PRIOR PLING DATE: 1999-05-21

PRIOR PLING DATE: 1999-05-21

PRIOR PLING DATE: 1999-05-22

PRIOR PLING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PARCHAIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                             67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                 8 CYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQ-P 66
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                                                                                                                                                                                                                                                                                                                                1 CKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGP
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                                                                                                                                                                                                Length 250;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                             Query Match 39.4%; Score 703; DB 10; Best Local Similarity 42.5%; Pred. No. 1.1e-53; Matches 127; Conservative 39; Mismatches 83;
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                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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61 WCYTTDPEKRYDYCDILECEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/10131241 Publication No. US20030012792A1
                                                   ORGANISM: Homo sapiens
     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-131-241-30
                                                                          IMMEDIATE SOURCE:
                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-131-241-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                           187 PSIRWEYCNITRCSDIEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 GOSYRGIFSTIVIGRICQSWSSWIPHRHQRIPENYPNDGLIMNYCRNPDADIGPWCFITD 186
                                                                                                                                               8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQ-P 66
                                                                                                                                                                                1 CXTGNGKNYRGTMSKTKNGIICQKWSSISPHRPRFSPAIHPSEGLEENYCRNPDNDPQGP 60
                                                                                                                                                                                                                                                                                            61 WCYTTDPEKRYDYCDILECEE-----ECMHCS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                 50;
                                              39.4%; Score 703; DB 9; Length 250; ilarity 42.5%; Pred. No. 1.1e-53; Conservative 39; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta STATE: Georgia COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: WATTOR OF WILLIAM L.
REGISTRATION UNDER: 36,714
REFERENCE/POCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application US/09335325
Patent No. US2020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 404-818-3799 INFORMATION FOR SEQ ID NO: 30:
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                                                                  Local Similarity
hes 127; Conserv
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US-09-335-325-30
US-09-761-120-30
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                                                   Query Match
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67 WCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGN 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 PSIRWEYCNLIRCSDIEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 GOSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADIGPWCFTID 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 PTKRWEYCDIPRC-----TTPPPP-----PSPTYQCLKGRGENYRGTVSVTVSGKT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 CQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 250;
                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPAGE OF SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                           STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.2%; Score 700; DB 10;
41.1%; Pred. No. 1.9e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REPERBUNCE/DOCKET NUMBER: 05213-0126
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPRAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US/08/612,788
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 29, 2003, 08:18:17 Job time : 349 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 WCYTTDPDKRYDYCNIPECEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                 FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                          COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                         & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 250 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 41.19
Matches 123; Conservative
                                                                CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICANT: FOLMELLY, Michael.

TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge FILE REPREBRE: 05940-0113 (43171-252068)

CURRENT APPLICATION NUMBER: 05/97/61,120

CURRENT FILING DATE: 2001-01-16

PRIOR PILING DATE: 1999-05-11

PRIOR PELILOGATION NUMBER: 08/866,735

PRIOR FILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.0

SEQ ID NO 29

LENGTH: 250
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                                              187 PSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTP 246
                                                                            WCYTTDPCVRWEYCNLIQCSETESGVLEIPIVVPVPSMEAHSEAAPTEQIPVVRQCYHGN 126
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                                                                                                                                      247 CQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLC 305
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Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: FOLYMAN, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.2%; Score 700; DB 9; Length 250; 41.1%; Pred. No. 1.9e-53; Live 37; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                         Sequence 29, Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature; CTHER INFORMATION: Kringle 1-3 US-09-761-120-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 123; Conserv
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September 29, 2003, 08:01:08; Search time 19 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                    using sw model
                                                                                      - protein search,
                                                                                         OM protein
                                                                                                                                 Run on:
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(without alignments) 1558.945 Million cell updates/sec 1786 1 KSPVVQDCYHGDGRSYRGIS.....TYMNPRKLFDYCDIPLCASS 308 283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-10-088-548-2 score: Scoring table: Perfect sc Sequence: Searched: Title:

160415 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 308

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	plasmin (EC 3.4.21	(EC 3.4	(EC 3.4	(EC 3	n a	OX40 homolog - hum	right origin-bindi	24K androgen-depen	attachment protein	transposase BMEI14	hypothetical prote	hypothetical prote	attachment protein	hypothetical prote	hypothetical prote	lectin-B - Virgini	immunoreactive pro	CD44 glycoprotein			chitinase (EC 3.2.	conserved hypothet	iolb protein [impo	Ig kappa chain V r	glutathione.peroxi	hypothetical prote	protein B0238.12 [major surface glyc	En/Spm-like transp
ID	A40522	E61545	C61545	A60140	I38098	I37552	AB1075	A47367	JQ1209	AB3430	A85231	T24703	JQ1208	T33698	T19913	JC5559	JC4589	D44355	\$24328	B49247	S65765	AI3110	C98176	S26475	S24327	H87524	H89044	MGNZ60	T52305
DB	10	7	~	~	7	7	~	7	7	~	7	7	7	~	N	7	N	~	,⊣	7	7	7	~	~	r~4	7	7	Н	7
Length	169	120	123	89	291	277	289	221	297	272	241	304	297	240	248	295	194	301	221	197	287		270	104	221	284	166	292	306
% Query Match	34.7	23.1	22.8	19.8	13.8	5.0	5.0	4.9	4.8	4.8	4.7	4.7	4.7	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.2	4.2
Score	620	413	408	354	246.5	88.5	٠	87.5	86.5		84.5	84.5	83.5	82	81	80	79.5	σ	79	78.5	78.5	78	78	77.5	77.5	77	92	75.5	75.5
Result No.	-	7	e	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

plasmin (EC 3.4.21.7) precursor - dog (fragments)
NiAlternate names: plasminogen
C;Species: Canis lugus familiaris (dog)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C;Accession: E61545
F;Schaller, J; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.

RESULT 2

whey acidic protei	glutathione peroxi	leucocyte common a	hypothetical prote	secretory protein	myo-inositol catab	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r	hypothetical prote	iolB protein [impo	major surface glyc	coccidiosis-relate	hypothetical prote	Ig kappa chain V r	Ig kappa chain V r
S01286	B40464	A45854	T28802	B40850	B69645	\$29584	S29592	S29581	T33597	AH3580	MGNZ18	A45517	A72648	S26459	S29587
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127	221	287	243	224	271	102	104	108	262	269	292	206	212	86	98
4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.	4	4.1	4.1	4.1
75	75	75	74.5	74	74	73.5	73.5	73.5	73.5	73.5	73.5	73	73	72.5	72.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A) Status: preliminary
A; Molecule type: mRNA
A; Cross-references: G: Molecule type: mRNA
A; Cross-references: G: Molecule type: Molecule type: mRNA
A; Note: the authors translated the codon TCT for residue 76 as Ala
C; Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homo: C; Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 34-112, Domain: kringle homology cKRG>
F; 34-112, 55-95, 83-107/Disulfide bonds: #status predicted
Disable (EC 3.4.21.7) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Battus norvegicus (Norway rat)
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C;Accession: A40522
R;Kanalas, J.J.; Makker, S.P.
B;Kanalas, J.J.; Makker, S.P.
A; Biol. Chem. 266, 10825-10829, 1991
A;Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor A;Reference number: A40522, MUID:91250378; PMID:1645711
A;Accession: A40522, MUID:91250378; PMID:1645711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDAD-IGPWCFITDPSIRWBYC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 RWEYCNLIQCSETESGVLETPIVVPVPSMEAHSEAAPIEQIPVVRQCYHGNGQSYRGIFS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 NLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATIVTGTPCQEWAAQE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.7%; Score 620; DB 2; Length 169; 61.0%; Pred. No. 5.1e-39; Live 14; Mismatches 43; Indels
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Best Local Similarity 61.09
Matches 111; Conservative
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168 PH 169
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t-plasminogen activator precursor,
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                                                                          55; Conservative
                                                    Similarity
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Best Local S:
Matches 80
                            Query Match
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Matches 5
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N;Alternate names: plasminogen
C;Species: Gallus gallus (chicken)
C;Species: A60140
R;Gyenes, M.; Patthy, I.
Biochim. Biophys. Acta 832, 326-330, 1985
A;Title: The Kringle 4 domain of chicken plasminogen.
A;Reference number: A60140; MUID:86077796; PMID:4074753
A;Accession: A6140
A;Accession: A6140
A;Accession: A6140
A;Accession: A6140
A;Residues: 1-89 cGTE>
C;Superfamily: plasminogen-related protein precursor homology
C;Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma: serine proteinase
F;6-83,20mahn: kringle homology cKRG>
F;6-83,27-66,55-78/Disulfide bonds: #status predicted
F;39/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disamin (EC 3.4.21.7) precursor - goat (fragments)
N;Alternate names: plasminogen
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C;Accession: C61545
N;Schaller, J.; Rickli, E.E.
Briyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Recession: C61545
A;Molecule type: protein
A;Residues: 1-123 <CSCH
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Repvords: hydrolase; serine proteinase
F;41-118/Domain: kringle homology <KR4>
                       A;Accession: E61545
A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-120 <SCH>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: hydrolase; serine proteinase
B;37-114/Pomain: kringle homology <KR4>
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                                                                                                                                                                                                                                                                                                     119 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 178
                                                                                                                                                                                                                                                                                                                             34 VQECTHGNGQSTRGTSSTIIGEKCQSWSSMIPHRHEKTPEHFPEAGLIMNYCRNPDADK 93
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0
                                                                                                                                                                                                           23.1%; Score 413; DB 2; Length 120;
larity 74.7%; Pred. No. 7.1e-24;
Conservative 12; Mismatches 10; Indels
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A; Reference number: A61545; MUID: 89005015; PMID: 3168975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 408; DB 2;
Pred. No. 1.7e-23;
9; Mismatches 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 YCRNPDADIGPWCFTTDPSIRWEYCNLTRCSD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 SPWCYTTDPSVRWEFCNLRKCLDPEAS 120
                                                                                                                                                                                                                                                                                                                                                                                              GPWCFTTDPSIRWEYCNLTRCSDTEGT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 22.8%;
l Similarity 73.9%;
68; Conservative
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Matches 68; Conserv
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                                                                                                                                                                                                                    Local Sime 65;
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NiAlternate names: tissue plasminogen activator (Species: Homo sapiens (man) (Cispecies: Homo sapiens (man) (Cispecies: Homo sapiens (man) (Cispecies: Homo sapiens (man) (Cispecies: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999 (Ciscossion: 138098; Solid'8 (Siebert P.D.; Pong, K. R. 1990 (R. Siebert P.D.; Pong, K. 1986, 1990 (R. Altitle: Variant tissue type plasminogen activator (PLAT) (CDNA obtained from human en A; Reference number: 138098; MUID:90192128; PMID:1969145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Cross-references: EMBL:X13097; NID:g35282; PIDN:CAA31489.1; PID:g35283
C;Comment: For the main splice form, see PIR:UKHUT. This form probably does not have
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cones. 205.1Mn.
A.Anthorons. Sp12-8p12
A.Anthorons. 24/3, 39/1; 87/1; 122/1; 180/2; 211/1; 268/2
A.Anthorons. 24/3, 39/1; 87/1; 122/1; 180/2; 211/1; 268/2
C.Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat C.Keywords: alternative splicing; fibrinolysis; glycoprotein; Kringle
F.1-23/Domain: signal sequence #status predicted <81G>
F.3-23/Domain: propeptide #status predicted <PGO<
F.33-291/Product: t-plasminogen activator, inactive endothelial splice form #status F.41-78/Domain: EGF homology <EGP>
F.117-208/Domain: EGF homology <EGP>
F.127-208/Domain: Kringle homology <ERIS
F.127-208/Domain: Kringle homology *RAIS
F.127-208/Domain: Kringle homology *RAIS
F.127-208/Domain: Kringle homology #status atypical <FR2>
F.127-208/JDomain: FR2>
F.127-208/JDomain: FR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 SYRGIFSTIVIGRICQSWSSMIPHRHQ---RTPENYPNDGLIM-----NYCRNPDADIGP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 WCFTTDP-SIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
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                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inactive endothelial splice form - human
                                                                                                                                                                                                                             121 QCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 RSYRGI---SSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 RSYQVICRDEKTQMIYQQHQSWLRPVLR-SNRVEYCWCNSGRAQCHSVPVKSCSEPRCFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 IDPCVRWEYCN--LTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHGNGQ
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26.2%; Pred, No. 3.7e-11;
.+ive 34; Mismatches 110; Indels
    Length 89;
19.8%; Score 354; DB 2; 67.9%; Pred. No. 1.2e-19;
                                                                                     11; Mismatches
                                                                                                                                                                                                                                                                                                                                                   181 WCFTTDPSIRWEYCNLTRCSD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: 138098
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-291 <SIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 WCYVFKAGKYSSEFCSTPACSE--
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97 SQTPALYRRSPEWSAFGIRPPLRLGEFTVPEHQFVTLEDTPLLGVTQSYS	Oy 68 CYTTDPCVRNETCKINGCESTESGVL	Species: Mus musculus (house mouse) Date: 21-Jan-1994 #sequence_revision Gayselinck, N.B.; Dufaure, I.; Lareyr I. Endocrinol. 7, 258-272, 1993 Ritle: Structural organization and re Reference number: A47367; MUID:932255 Accession: A47367 Status: preliminary Robiccule type: nucleic acid Residues: 1-221 <ghy> Experimental source: BALB/C</ghy>	oce inconsistent with more extracted from WC N.B.; Dufaure, J.P. Res. 18, 7144, 1990 Res. 0NA sequence for manber: \$13725; MUID:913725 Re: mRNA -52, /H', 54-102, 'Q', Jances: EMBL:X53780; N. equutathione peroxid	., 85 85	RESULT 9 JO1209 attachment protein - human respiratory syncytial virus (strain RSB6614) N;Alternate names: G protein C;Species: human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Date: 31-War-1992 #sequence_revision 31-War-1992 #text_change 16-Feb-1997 C;Accession: JO1209 R;Cane, P.A.; Matthews, D.A.; Pringle, C.R. J, Gen. Virol. 72, 2091-2096, 1991 A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JO1204; MUID:91374005; PMID:1895054	A; Accession: JQ1209 A; Molecule type: mRNA A; Residues: 1-297 CCANA> C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory tracter children and adults. C; Superfamily: respiratory syncytial virus major surface glycoprotein G
Db 279 ASMRP 283	RESULT 6 13752 CX40 homolog - human CX5pecies: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 13752 C;Accession: 13755 C;Accession: 1	Query Match S.08; Score 88.5; DB 2; Length 277; Best Local Similarity 19.08; Pred. No.17; Matches 51; Conservative 31; Mismatches 89; Indels 97; Gaps 12; QY 18 SISTITYTERTCCSWSZMIPHWHORTPRNYPNAGLTENYCRNPDSGKQPWC 68 1	QY 120 RQCYHGNGQSYRGTFSTTVTGRTCQSWSSMT-PHRHQRTPENTPNDGLTMNYCRNPDADT 178 Db	RESULT 7 AB1075 right origin-binding protein [imported] - Salmonella enterica subsp. enterica serovar Ty C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Dacession: AB1075 R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, Nature 413, 848-852, 2001	A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A; Reference number: ABD502; MUID:21534947; PMID:11677608 A; Accession: AB1075 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-289 cPAR> A; Cross-references: GB:AL513382; PIDN:CAD03417.1; PID:g16505685; GSPDB:GN00176 C; Genetics: A; Gene: STY4933	Query Match 5.0%; Score 88.5; DB 2; Length 289; Best Local Similarity 22.7%; Pred. No. 18; Matches 48; Conservative 18; Mismatches 60; Indels 85; Gaps 10; Qy 20 SSTIVIGRICQSWSSMIPHWHQRIPENYPRNAGLIENYCRNPDSGKQPW 67

RESULT 11 A85231 hyporthetical protein AF4g20350 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C; Accession: A85211 R; anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Accession: A85001; WUID:20083488; PMID:10617198 A; Status: preliminary	A; Molecule type: DNA A; Residues: 1-241 <sto> A; Cross-references: GB:NC_001268; NID:97268830; PIDN:CAB79035.1; GSPDB:GN00140 C; Genetics: A; Gene: AT4920350 A; Map position: 4 Query Match Best Local Similarity 21.8%; Score 84.5; DB 2; Length 241; Best Local Similarity 21.8%; Pred. No. 29;</sto>	WATCHES 4.2; CONSGIVATIVE 15; MISHBALCHES 70; AGES 95 TPTVVPVPSABAHSEAAPTEQTPVVRQCYHGNGGSYRGTPSTTVTGRTCQSWSSMTPHRH 15 11 TPTVFYIPGFIIDEEQTQLLNHIYGASGSKWKTLKNRRLQNWGGWV-HEK 59 155 QRTPENYP	CNLTRCSDTEGTVVAPPTVIQVBSLGPPSEQDCMFGKGKKATTVTGTPCQE CNLTRCSDTEGTVVAPPTVIQVBSLGPPSEQDCMFGKGKKATTVTGTPCQE : :	RESULT 12 724703 hypothetical protein T08G3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: 7124703 R;Lloyd, C. R;Lloyd, C. Submitted to the EMB1 Data Library, December 1996	A, Accession: T24703 A, Accession: T24703 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNBA A, Residues: 1-304 < WILD A, Cross-references: EMBL: 283238; PIDN: CAB05796.1; GSPDB: GN00023; CESP: T08G3.6 A, Experimental source: clone T08G3 C, Genetics: A, Gene: CESP: T08G3.6 A, Gene: CESP: T08G3.6 A, Consistion: 5 A, Introns: 86/2	Ouery Match Best Local Similarity 19.1%; Pred. No. 37; Matches 53; Conservative 33; Mismatches 108; Indels 83; Gaps . 14; Qy RTERSGVLETPLYVPYPSMEAHSEAAPTEQTPVVRQC 122	QY 123 YHGNGQSYRGIFSTTVTGRICQSWSSMTPHRHQRIPENYPND 164
<pre>Geywords: glycoprotein; transmembrane protein 15,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #s 15,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #s wery Match 4</pre>	Db 133TKNTTTTQIQP-SKPTTKQHQNKPPNKPNNHFHFEVFNFVPCSICSNNPTC 182 QY 183 FTIDPSIKWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSE 223 183 WAICKRIPNKKPGKKTTTKPTKRTIKTTKKDLKPQTTKPKEVLTTKPTE 232 QY 224 QDCMFGNGKGYRGKKATT-VTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGD 282 234 KPTINTTKTNIRTLLTTNTTGNPEYTSQKETLHSTSPEGN 273	3 INGPWCYT 290 4 PSPSQVYT 281	Langaboase mailter Imported Firefile Mellelia C.Species: Brucella melitensis C.Species: Olembar ABS430 C.Species: C.Species: ABS430 C.Species: ABS430 C.Species: ABS430 C.Species: A.Species:	R> : strain 16M	QUELY MATCH 4.4%; SOOZE 85.5; DB 2; Length 272; Best Local Similarity 21.8%; Pred. No. 28; Matches 62; Conservative 29; Mismatches 77; Indels 117; Gaps 18; QY 30 QSWSXMPHWARTPENTPRAGLENYCRNPDSGKOPWCTTDPCV- 75 Db 10 QQWAVIAPLLPTWQPGAHRTDDRRVISGIIHILRSGCRWQDCPACYGPPTTVY 62 QY 76RWBYCNLTQCSETESGVLETPTVVPVPSWEAHSEAA	OY 112PTEQTEVVRQCYHGNGQSYRGTFSTTVTGRT 142	QY 189'IRWEYCNLTRCSDTEGTVVARPTVIQVPSLGPPSEQ 224 :: :

A; Experimental source: strain Bristol N2; clone F49F1 C; Genetics: A; Gene: CESP:F49F1.7 A; Map position: 4 A; Introns: 42/2; 79/2; 116/2; 209/2 C; Superfamily: Caenorhabditis elegans hypothetical protein F49F1.6 Cuery Match Best Local Similarity 21.1%; Pred. No. 44; Matches 44; Conservative 17; Mismatches 74; Indels 74; Gaps 9; Matches 28 TQCSWSMIPHWHQRTPENYCRNPOGGEQPWCYTTDECVRWBYCNI 82 C)	Db 57 TCSDINGDCEKFHEMCVMMPYREQCPKSCGICDSPAPTWCMDHWPECPK 105 QY 83 TQCSETE	RESULT 15 T19913 hypothetical protein C43F9.5 - Caenorhabditis elegans C; Species: Gaenorhabditis elegans C; Species: Gaenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T19913 R; Mortinore B. Submitted to the EMBL Data Library, November 1996 A; Reference number: Z19195 A; Accession: T19913 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	A; Residues: 1-248 <wiid> A; Residues: 1-248 <wiid> A; Cross-references: EMBL:282262; PIDN:CAB05152.1; GSPDB:GN00022; CESP:C43F9.5 A; Experimental source: clone C43F9 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; T8/3; 118/1; 199/3 A; Map position: 4 A; Introns: 47/1; 78/3; 118/1; 199/3 Query Match Est Local Similarity 23.8%; Pred. No. 55; Matches 59; Conservative 19; Mismatches 114; Indels 56; Gaps 15;</wiid></wiid>	QY 13 GRSYRGISSTTVTGRTCQSWSANIPHWHORTPRNYPNAGLTENYCRNPDSGKQPW 67	QY 125 GNGQSXRGTEST-TVTGRTCQSWSSMTPHRHQRTPENYPNDGL-TMNYCRNPDADTGP 180
QY 165 GLEMNYCRNPDADTGPWCFITDPSIRMEYCNLFRCSDTEGTVVAP 209 143 GFWSTWSATRRDGEKRAWSRTRRCLTEEAGCPCTDPGTIETSTACFIKLUDVSSLV 200 QY 210 PTVIQVPSIGPP-SEDDCKFGNGKGYRGKKATTVTGTPCOEMAAQEPHRHSTFIPG 264 1 :: ::: :::	dno.	rer respiratory tract illotein G valent) #status predict 77, Gaps 13; PPVVRQCYHG 125 11: 11: 11: 11: 11: 11: 11: 11: 11: 11	Qy 126 NGOSYRGTESTTUTGRICOSWSSMTPHRHORIPENYPUDGLTMNYCRNPDADJGPWC 182	QY 283 INGPWCYT 290 Db 274 PSPSQVYT 281 RESULT 14	Pysobhetical protein F49F1.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change O8-Sep-2000 C;Accession: T33698 F;Miller, N.; Wamaley, P. Submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid F49F1. A;Reference number: Z21389 A;Accession: T33698 A;Status: preliminary; translated from GB/EMBL/DDEJ A;Mesidues: 1-240 <mil.> A;Residues: 1-240 <mil.> A;Cross-references: EMBL:AP100656; PIDN:AAC68946.1; GSPDB:GN00022; CESP:F49F1.7</mil.></mil.>

Search completed: September 29, 2003, 08:04:08 Job time: 23 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUR4_HUMAN

ID TUR4_HUMAN

STANDARD; PRT; 277 AA.

AC P41489; Q13663;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 12, Last annotation update)

DE TUROR necrosis factor receptor superfamily member 4 precursor (OX40L DE receptor) (ACT95 antigen) (TAX-transcriptionally activated GN TURENST4 OR TXGELL.
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**MEDLINES-94170844; PubMed=7510240;

**MEDLINES-94170844; PubMed=7510240;

**Howmel M., Fonatsch C., Stein H.;

**The human OX40 homolog: oDNA structure, expression and chromosomal assignment of the Acriss antigen.";

**Bur. J. Immunol. 24:677-683(1994).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS0010; KRINGLE_2; 2.
PROSITE; PS00140; TRYPSIN_LDOM; PARTIAL.
PROSITE; PS00134; TRYPSIN_SIN_LHIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SIN_PRATIAL.
Bydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Kawamate S., Hori T., Imura A., Takaori-Kondo A., Uchiyama T.;

"Activation of Ox40 signal transduction pathways leads to tumor

"Activation of Ox40 signal transduction pathways leads to tumor

"Activation of Ox40 signal transduction pathways leads to tumor

"TRAF5-mediated NF kappaB activation.";

"Biol. Chem. 273:808-5814(1998).

"IFRAF5-mediated NF kappaB activation.";

"SBOUIT: Interacts with TRAF5.

"SUBJUIT: Interacts with TRAF5.

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"WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                        Pankow R., Duerkop H., Latza U., Krause H., Kunzendorf U., Pohl T.,
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SMART, SM00208; TNFR. 3.
PROSITE; PS00652; TNFR_MGFR_1; 2.
PROSITE; PS50060; TNFR_MGFR_2; 2.
Receptor; Antigen; Transmembrane; Glycoprotein; Repeat; Signal.
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EMBL, S76792, AAB33944.1; ALT_INIT.

EMBL, AJ71151; CAB96543.1; -.

FMRL, AJ77152; I37552.

HSSP, O14763; 1D06.

GOOW, HORGIL1918, TNPRSP4.

MIM; 600315; -.

GO; GO:0005687; C:integral to plasma membrane; TAS.

GO; GO:00005027; F:NGF7NR (6 C-domain) receptor activity; TAS.

GO: GO:0006555; P:Immune response; TAS.

InterPro; IPR001368; TNFR_C6.
                                                                                                                                           "The HTLV-I protein transcriptionally modulates OX40 antigen expression.";
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TWER-CYS 3 (INCOMPLETE).
TWER-CYS 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR-CYS 1.
                                                                                                                                                                                                                                                                          INTERACTION WITH TRAF1; TRAF2 AND TRAF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
[3]
SEQUENCE FROM N.A.
MEDLINE=20318724; PubMed=10861060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH TRAF2 AND TRAFS.
                                                                                                                                                                                                          J. Immunol. 165:263-270(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
2235
277
277
1007
1007
1007
1007
141
                                                                                                                        Bulfone-Paus S.;
                                                                                                                                                                                                                                                                                                         PubMed=9418902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9488716;
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18

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SEQUENCE

SET

Query Match

DISULFID CARBOHYD CARBOHYD 131

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166

VGLG_HRSV7 RESULT 3

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                                                                                                                                                                                                                                                                                                                                             -----SPEGN 273
                                                                                                                            126 NGQSTRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGL---TMNYCRNPDADTGPWC 182
                                                                                                                                                                                                                -TIDPSIRWEYCNLIRCSDIEGTVVAPPTVIQVPSLGPPSE 223
                                                                                                                                                                                                                                                                                                   224 QDCMFGNGKGYRGKKATT-VTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Protects cells and enzymes from oxidative damage, by catalyzing the reduction of hydrogen peroxide, lipid peroxides and organic hydroperoxide, by glutathione. May constitute a glutathionine peroxidase-like protective system against peroxide damage in sperm membrane lipids.
-!- CATALYTIC ACTIVITY: 2 glutathione + H(2)0(2) = oxidized glutathione + E(2)0.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SINCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EPIDIDIMIS.
                                         PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHG
                                                                                88 PIYLIQUPQLGISFSNL---SETTSQPATTPALT-TPSAES----TPQSTTVK----
                                                                                                                                                     TISSUB-Epididymis;
MEDLINE-92004864; PubMed=1913244;
Ghyselinck N.B., Rigaudiere N., Dufaure J.-P.;
Androgen-dependent protein secreted by mouse caput epididymis shows high homologies with different glutathione peroxidases.";
C. R. Acad. Sci., III, Sci. Vie 313:1-6(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Epididdymal secretory glutathione peroxidase precursor (BC 1.11.1.9)
(Epididymis-specific glutathione peroxidase-like protein) (EGLP)
(Major androgen-regulated protein) (ARMEP24).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Manmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins
77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Epididymis;
MEDLINE-91088305. PubMed-2263479;
Ghyselinck N.B., Dufaure J.-P.;
Ghyselinck N.B., Dufaure J.-P.;
A mouse colks sequence for epididymal androgen-regulated prelated to glutathione peroxidase.";
Nucleic Acids Res. 18:7144-7144(1990).
-!- FUNCTION: Protects cells and enzymes from oxidative da catalyzing the reduction of hydrogen peroxide, lipid p
Indels
88;
                                                                                                                                                                                                                                                                                                                            221 AA.
Mismatches
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 47-221 FROM N.A.
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          283 INGPWCYT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      274 PSPSQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                   183 F-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSHE_MOUSE
                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSHE_MOUSE
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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                                             QΫ
                                                                                                                                                                                                                QΥ
                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                   69 -YTIDPCVRWEYCNLIQCSETESGVLETPTVV-----PVPSMEAHSEAAPTEQTPVV 119
                                                                                                                                                                                                                                                                                                                   75 VVSSKPCKPCIWCNLRSGSBRKQLCTAIQDIVCRCRAGIQPIDSYKPGVDCAPCPP---- 130
                                                                                                                                                                                                                                                                                                                                                                        120 RQCYHGNGQSYRGTFSTTVTGRTCQSWSSMT-PHRHQRTPENYPNDGLTMNYCRNPDADT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- 183
                                                                                                                                                                                                68
                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOUSTICE FROM N.A.
MEDITURE-91374005; PubMed-1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Matthews D.A., Pringle C.R.;
Cane P.A., Mattheation of variable domains of the attachment (G) protein of subgroup A respiratory syrcytical viruses.",
J. Gen. Virol. 72:2091-2096(1991).
-!- FUNCTION: UNILEE THE OTHER PARAMIXOVIBUS ATTACHMENT PROTEINS, THE REPIRADORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                          20 GLGLSTYTGLECYGDTYPSNDRCCHECRPGN----GMVSRCSRSQNTVCRP-CGPGFYND
                                                                                                                                                                                                GISSTTVTGRTC--QSWSSMIPHWQRTPENYPNAGLTENYCRNPDSGKQPWC-----
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLUTAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-i- PTH: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
PIR; JQ1209; JQ1209.
                                                                                                                                                                                                                                                                                                                                                                                                               ------GHFSPG-DNQACKPWINCILAGKHILQPASNSSDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. ..) (POTENTIAL).
166 BY SIMILARITY.
146 N-LINKED (GLCNAC. ..) (POTENTIAL)
160 N-LINKED (GLCNAC. ..) (POTENTIAL)
29340 MM, 49FISS2S4ISSOBF CRC64,
                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 297;
                                                                                                           DB 1; Length 277;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .LINKED (GLCNAC. . .) (PG 58B384028E437ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PPATQPQETQGPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus (strain rsb6614)
                                                                                                                                                     89
                                                                                         Score 88.5; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86.5; DE
Pred. No. 5.4;
                                                                                                                                Pred. No. 3.5;
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ATTVTGTPCQEW--AAQEPHRHSTFIPG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ARPITVQPTEAWPRTSQGPSTRPVEVPG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000925; Glycoprot_G. Pfam; PF00802; Glycoprotein_G; 1. Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32670 MW;
                                                                                                           5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%;
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
103
135
237
251
294
147
146
160
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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                                                                                                                                  Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGLG_HRSV7
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DOMAIN TRANSMEM

CARBOHYD CARBOHYD

SEQUENCE Query Match

CARBOHYD

DOMAIN

13;

125

182 223 232

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                                                                                                                                                                                                                 126 NGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGL---TMNYCRNPDADTGPWC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 KPTINITERILETINITGNP--EYISQKETLHST-----SPEGN 273
                                                                                                                                                           88 PTYLTQNPQLGISFSNL---SETTS----QPTTTPAPTTPS---AESTPQSTTVK---- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                      224 QDCMFGNGKGYRGKKAIT-VIGIPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Protects cells and enzymes from oxidative damage, by catalyzing the reduction of hydrogen peroxide, lipid peroxides and organic hydroperoxide, by glutathione. May constitute a glutathionine peroxidase-like protective system against peroxide damage in sperm membrane lipids.
-: CAPALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + D H(2)O.
-: SUBCELLUAR LOCATION: Secreted.
-: SUBCELLUAR: LOCATION: Secreted.
-: TISSUE SPECIFICITY: EPIDIDIMIS.
-: SIMILARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                                                                                                                                 183 F------TIDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSE
                                                                                                          PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYHG
                                                                                                                                                                                                                                                                        133 -----IKNTITI--QIQP-SKPITKQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTC
                                                                                                                                                                                                                                                                                                                                                                                  183 WAICKRIPNKKPGKKTTTKPTKKPTIK-----TTKKDLKPOTTKPKEVLTT----KPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
Epididymal secretory glutathione peroxidase precursor (EC 1.11.1.9)
(Epididymis-specific glutathione peroxidase-like protein) (EGLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Wistar; TISSUB-Epididymis; MEDLINE-82359957; PubMed=1386734; Perry A.C.F. Jones R., Miang L.S.P., Jackson R.M., Hall L.; Generic evidence for an androgen-regulated epididymal secretory quitathione peroxidase whose transcript does not contain a selenocysteine_codon_";
                                                      77;
                                                      89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00435; IGP1.
InterPro; IPR0000889; Glut_peroxidase.
Pfam, PP00255; GSHPx; 1.
PRINTS; PR01011; GLUTPROXDASE.
PROSITE; PS00460; GLUTATHIONE_PEROXID_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AA.
                         Pred. No. 9.3;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
22.6%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. J. 285:863-870(1992).
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                            Similarity 22.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 INGPWCYT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 PSPSQVYT 281
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                                                                                                             99
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                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
GSHE_RAT
                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 YCNLTRCSDIEGIVVAPPIVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 YCGLT------LVILGFPCNQFGK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subgroup A respiratory syncytial viruses.",

J. Gen. Virol. 72:2091-2095(1991).

1. Gen. Virol. 72:2091-2095(1991).

FEDETRATORY SINCYTIAL OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SINCYTIAL OTHER PRAMYXOVIRUS ATTACHMENT PROTEINS.

1- FURCHIOTINATING ACTIVITIES.

1- SUBCELLULAR LOCATION: EXPRESSED ON THE SUBPACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

1- FPRI. MY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.

PIR, J01208; J01208

FIRMINGS, Glycoprotein.6; 1.

Transmembrane; Glycoprotein.6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLUIAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 QEPHRHSTFIPG---TNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDY 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. EPIDIDYMAL SECRETORY GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.7%; Score 84.5; DB 1; Length 221; 25.5%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; šsRNA nēgativē-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11256;
                                                                                                                                                                                                                                                                                                                                                                                           PEROXIDASE.
BY SIMILARITY.
D -> H (IN REF. 2).
DE5F8BD6CD22D6F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6781756C38B64A80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus (strain rsb6256).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                       MGD; MGI:104886; Gpx5.
InterPro; IPR000889; Glut_peroxidase.
Pfam; PF00255; GSHPx; 1.
PRINTS; PR01011; GLUTPROXDASE.
PROSITE; PS00460; GLUTPROXDASE.
PROSITE; PS00460; GLUTPROXDASE.
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                                                                                                                                                                                                                                                                                                                Oxidoreductase; Peroxidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91374005; PubMed=1895054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                     73 B
53 D
25381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.78;
                                                            EMBL; X53780; CAA37796.1; -.
                                  EMBL; M68896; AAA37729.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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103
103
135
237
251
                                                                                      PIR; A47367; A47367.
HSSP; P00435; 1GP1.
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67
103
135
237
251
294
297 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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28;
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CARBOHYD
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VGLG_HRSV6
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A37077; MGNZ60.
InterPror, IPRO00325; Glycoprot_G.
Pfam: PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein_G; 1.
                                                                   73 BY
25212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55633; AAA47413.1; -. EMBL; M73545; AAA47408.1; -.
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                 72 YCGLT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
66
292
  21
                                                                                          221 AA;
                                                                                                                                                 Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                   73
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01-NOV-1991 (
01-AUG-1992 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGLG_HRSV8
                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                 193 YCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAA 252
                                                                                                                                                                                                                                                                                             72 YGGLT-----LVILGFPCNQFGX 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blochem. J. 285:863-870(1992).

-1- FUNCTION: Protects cells and enzymes from oxidative damage, by catalyzing the reduction of hydrogen peroxide, lipid peroxides and organic hydroperoxide, by glutathione. May constitute a glutathionine peroxidase-like protective system against peroxide damage in sperm membrane lipids.

-1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized glutathione + 2 H(2)O(2) = oxidized glutathione + 2 H(2)O(2) = oxidized glutathione + 2 H(2)O(2) = oxidized glutathione PERORIGITY: SPIDIDYMIS.
-1- SIMILARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Epididymal secretory glutathione peroxidase precursor (EC 1.11.1.9)
(Epididymis-specific glutathione peroxidase-like protein) (EGLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perry A.C.F., Jones R., Niang L.S.P., Jackson R.M., Hall L.; "Genetic evidence for an androgen-regulated epididymal secretory glutathione peroxidase whose transcript does not contain a selenocysteine codon.";
                                                                                                                                                                                                                         28;
                                                                     EPIDIDYMAL SECRETORY GLUTATHIONE
                                                                                                                                                                         Score 79; DB 1; Length 221;
Pred. No. 15;
9; Mismatches 35; Indels
                                                                                                          BY SIMILARITY.
0D9D3FAAC9F12D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              107 QEPGDNTEILPGLKYVRPGKGFLPNFQLFAKGDVNG 142
                                                                                                                                                                                                                                                                                                                                                    253 QEPHRHSTFIPG---INKWAGLEKNYCRNPDGDING 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P00435; IGP1.
InterPro; IPR000889; Glut_peroxidase,
Pfam; PP00255; GSHEX; 1.
PRINTS; PR01011; GLUTPROXDASE.
PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
Oxidoreductase; Peroxidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AA.
GLUTATHIONE_PEROXID_2; 1.
                                                                                        PEROXIDASE
                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                       Oxidoreductase; Peroxidase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Epididymis;
MEDLINE=92359957; PubMed=1386734;
                                                                                                          73 B: 25384 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62403; CAA44273.1; -.
                                                                                                                                                                           Query Match 4.4%;
Best Local Similarity 25.0%;
                                                                                                                                                                                                                       24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S24327; S24327.
                                                                                                                                 221 AA;
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SEQUENCE FROM N.A.
PROSITE; PS00763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9541;
                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSHE_MACFA
                                                                                                            ACT_SITE
SEQUENCE
                                                                                                                                                                           Query Match
                                            SIGNAL
                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSHE_MACFA
                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                 193 YCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAA 252
                                                                                                                                                                                                                                                                                               ----AQYPELNALQEELKPYG-----LVVLGFPCNQFGK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sullender W.M., Anderson K., Wertz G.W.;
"The respiratory syncytial virus subgroup B attachment glycoprotein: analysis of sequence, expression from a recombinant vector, and evaluation as an immunogen against homologous and heterologous subgroup virus challenge.";
Virology 178:195-203(1990).
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                         253 QEPHRHSTFIPG---TNKWAGLEKNYCRNPDGDINGPWCYIMNPRKLFDY 299
                                                                                                                                                                                       33;
EPIDIDYMAL SECRETORY GLUTATHIONE PEROXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus (subgroup B / strain 8/60).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11258;
                                                                                                                                     DB 1; Length 221;
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. EXTRACELLULAR (POTENTIAL).
                                                       BY SIMILARITY.
32AE912ED6C73D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AA
                                                                                                                               4.3%; Score 77.5; I 23.6%; Pred. No. 20; Eive 11; Mismatches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                       57 CRNPDSGKQPWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 CPEPSSSEETLCLSDNDCLGSTVC----CPSAAGGSCRTPIIVPTPK----AGRCPWVQA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID-10116;
                                         InterPro; IPR002221; WAP.
Priam; PF00035; Wap; 2.
SMART; SM00217; WAP. 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
PROSITE; Protease inhibitor; Repeat; Phosphorylation; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Glutathione peroxidase RY2D1 precursor (EC 1.11.1.9) (Odorant-metabolizing protein RY2D1).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - TISSUE SPECIFICITY: EXPRESSED IN THE BOWMAN'S GLANDS.
-i - SINITARITY: Belongs to the glutathione peroxidase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-Olfactory epithelium;

MEDLINE-92031476; PubMed=1931961;

MEDLINE-92031476; PubMed=1931961;

Molecular Cloning of putative odorant-binding and odorant-metabolizing proteins.";

Biochemistry 30:10376-10382(1991).

-! CARLEYTIC ACTIVITY: 2 glutathione + H(2)0(2) = oxidized glutathione + 2 H(2)0.
-! SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                             Score 75; DB 1; Length 127; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                          PHOSPHORYLATION (PROBABLE). 59DAD5FBFD2E2087 CRC64;
                                                                                                                                                                                                           WHEY ACIDIC PROTEIN
                                                                                                                                                                                                                                 WAP 1 (ATYPICAL). WAP 2 (ATYPICAL).
                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- --
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PROSITE; PSO0460; GLUTATHIONE_PEROXID_1;
PROSITE; PSO0763; GLOTATHIONE_PEROXID_2;
OLOGIQUE STATE STATE
                                                                                                                                                                                                                                                                                                                                                                       Pred. No
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InterPro; IPR000889; Glut_peroxidase.
Pfam; PF00255; GSHPx; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                      19
127
18 68
121 '
737
13526 MW; 5
                                                                                                                                                                                                                                                                                                                                                 4.2%;
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.2 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; B40464; B40464.
PIR; S01286; S01286.
HSSP; O46655; 1CJH.
                                                                                                                                                                                                      20
28
74
74
237
127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 PVVRQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMLSQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSHY_RAT
Q64625;
                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSHY_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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                                                                                                                                                                 10;
                                                                                                                                                                                                                                                            69 VILTIVIVQTIKNHIGKNISIYLIQVP-----PERV------NSSKQP---T 106
                                                                                                                                                                                                                                                                                                        71 IDPCVRWEYCNLIQCSETES-----GVLETPTVVPVPSWEAHSEAAPTEQTPVVRQC 122
                                                                                                                                                                                                                                                                                                                                   163 YHFEVPNFVPCSICGNNQLCKSICKTIPSNKPKKKPTIKPTNKPTTKTUKRDPKTPAKM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 PNDGLIMNYCRNP----DADIGPWCFTIDPSIRWEYCNLIRCSDIEGTVVAPPIVIQVP 216
                                                                                                                                                                                                                                                                                                                                                                                                  123 YH-----GNGQSYRGTFSTTVTGR-----TCQSWSSMTPHRHQRTPENY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 PKKEIITNPTKKPTLKTTERDISTSQSTVIDTITPKY-TIQQQSLHSTTSENTPSSTQIP 281
                                                                                                                                                                                                             19 ISSTIV-----TGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPWCYT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN COMPONENT OF MILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Mammary gland; MEDILINE-88335562; PubMed-3419910; MEDILINE-88335562; PubMed-3419910; Devinoy E., Hubert C., Schaerer E., Houdebine L.M., Kraehenbuhl J.P.; Sequence of the rabbit Whey acidic protein cDNA."; Nucleic Acids Res. 16:8180-8180(1988).
                                                                                                                                                                 69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90301490; PubMed-2362817;
Thepot D., Devinoy E., Fontaine M.L., Hubert C., Houdebine L.M.;
"Complete sequence of the rabbit whey acidic protein gene.";
Nucleic Acids Res. 18:3641-3641(1990).
81 N-LINKED (GLCNAC. . .) (POTENTIAL).
86 N-LINKED (GLCNAC. . .) (POTENTIAL).
1100 N-LINKED (GLCNAC. . . (POTENTIAL).
32143 MW, 8ECGC85EFG57BBS CRC64,
                                                                                                         Score 75.5; DB 1; Length 292; Pred. No. 39;
                                                                                                                                                                 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: COULD BE A PROTEASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: EIGHT DISULFIDE BONDS ARE PRESENT. -!- SIMILARITY: Contains 2 WAP-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 AA.
                                                                                                                                                               37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whey acidic protein precursor (WAP)
                                                                                                                     4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52564; CAA36798.1; -. EMBL; X07943; CAA30764.1; -.
                                                                                                                                                                    48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
81
86
100
292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 SLGPPS 222
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TASEPS 287
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAP_RABIT
P09412;
  CARBOHYD
                          CARBOHYD
                                                     CARBOHYD
                                                                         SEQUENCE
                                                                                                                                              Best Loc
Matches
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XP4_XENLA
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SEQUENCE
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                                                                              Best Loc
Matches
                                                                                                                                                                                                                               RESULT 12
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                                                                                                    -----TVTGTPCQEWAAQEPHRHSTFIPG---TNK 267
                                                                                                                   plutethione peroxidase-like protein secreted in the porcine epididymal fluid.";
Blochim. Blochim. Blochis. Acta 1336:99-109(1997).
-!- FUNCTION: MAY CONSTITUTE A GLUTATHIONINE PEROXIDASE-LIKE PROTECTIVE SYSTEM AGAINST PEROXIDE DANAGE IN SPERM MEMBRANE LIPIDS. SINCE THE PUBLIED PORCINE BNAYME HAS VERY LITLE ACTIVITY TOWARDS HYDROGEN PEROXIDE OR ORGANIC HUDROPEROXIDES THE PROTECTIVE EFFECT IS NOT LIKELY TO BE SEXEMED BY ITS ENERMATIC ACTIVITY. INSTEAD, MAY PROTECT SPERM FROM PREMATURE ACROSOME REACTION IN THE
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Last sequence update)
30-MAR-2000 (Rel. 39, Last annotation update)
Epididymal secretory glutathione peroxidase precursor (EC 1.11.1.9)
(Epididymis-specific glutathione peroxidase-like protein) (EGLP).
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Epididymis;
MEDLINE-97416456; PubMed-9271255;
MEDLINE-97416456; PubMed-9271255;
Okamura N., Iwaki Y., Hiramoto S., Tamba M., Bannai S., Sugita Y.,
Syntin P., Dacheux F., Dacheux J.L.,
"Molecular cloning and characterization of the epididymis-specific
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: PROXIMAL CAPUT EPIDIDYMIS.
-!- SIMILARITY: Belongs to the glutathione peroxidase family.
GLUTATHIONE PEROXIDASE RYZD1.
                                                   DB 1; Length 221;
                                                                           13; Mismatches 32; Indels
                           92749EAF6A3EF48C CRC64;
                                                                                                                                                    268 WAGLEKNYCRNPDGDINGPWCYTMNPRKLFDY 299
                                                                                                                                                                           125 GGGFVPNFQLFEKGDVNGD----NEQKVFSF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIMES, PRO1011, GLUTPROXDASE.
PROSITE; PRO1016, GLUTATHIONE_PEROXID_1; 1.
PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
Oxidoreductase; Peroxidase; Signal.
SIGNAL
                                                                                                                                                                                                                                           219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 22-46.
           BY SIMILARITY
                                                   Score 75;
                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000889; Glut_peroxidase.
Pfam; PF00255; GSHPx; 1.
                                                                                                                                                                                                                                                                 15-JUL 1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                    227 MFGNGKGYRGKKAT-----
22 221 G
73 73 B
221 AA; 24961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D37916; BAA22149.1; -. HSSP; P00435; 1GP1.
                                                               25.0%;
                                                                           23; Conservative
                                                                                                                                                                                                                                           STANDARD;
                                                 Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                           GSHE_PIG
              ACT_SITE
                           SEQUENCE
                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                            193 YCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 YCGLT------LVVLGFPCNQFELKPFG-----LVVLGFPCNQFGK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hauser F., Hoffmann W.; "xPl and xP4. P-domain peptides expressed in Xenopus laevis stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (African clawed frog).
17-SEP-2003 (African clawed frog).
18-SEP-2003 (
                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 QEPHRHSTFIPG---TNKWAGLEKNYCRNPDGDINGPWCYTMNPRKLFDY 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUTATIVE GASTROINTESTINAL GROWTH
EPIDIDYMAL SECRETORY GLUTATHIONE
                                                                                                                                                                                                                                DB 1; Length 219;
                                      PEROXIDASE.
BY SIMILARITY.
A22850A6477A262D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- TISSUE SPECIFICITY: STOMACH MUCOSA.
-- PTM: GLYCOSYLATED.
-- SIMILARITY: Contains 4 P-type (trefoil) domains.
                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Repeat.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                           4.2%; Score 74.5; D
24.5%; Pred. No. 34;
iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mucosa.";
J. Biol. Chem. 266:21306-21309(1991).
-i- FUNCTION: MAY ACT AS A GROWTH FACTOR.
-:- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR XP4.
P-TYPE 1.
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P-TYPE 3.
P-TYPE 4.
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MEDLINE=92042013; PubMed=1939167;
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Signal, Growth factor; Glycoprot
SIGNAL 1 17 POI
CHAIN 18 224 PUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04155; 1PS2.
InterPro: IRN000519; P_trefoil.
Pfam; PF00088; trefoil; 4.
SMART; SM00018; PD; 4.
                                                                                     71 B:
24936 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M75034; AAA50003.1; -. PIR; B40850; B40850.
                                                                                                                                                                                                                                                                           Local Similarity 24.5
hes 27; Conservative
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116
116
215
215
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52
102
102
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224 ODCMFGNGKGYRGKKALTVTGTPCQEW 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Fr. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 439124; CABLOLILI,
EMBL; ABO05554; BAA21610.1; -.
PIR; B69645; B69648.
Subtilist; BG11118; iolb.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D14399; BAA03291.1; -. EMBL; Z99124; CAB16011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTFSTTVTGRT - - - - -
                                                                                                                                                   SEQUENCE OF 1-71 FROM N.A.
                                                                                                                       Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                  / BGSC1A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteome.
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                                                                                                                                                                  STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete p
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Matches 4
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LD VGLG_HRSV1

AC P20896

DT 01-FEE

DT 01-FEE

DT 01-FEE

DT 01-KDE

GO NOINGE

OC Virus-
OC Virus-
OC NCBL

RN [1]

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RN SEQUE

RR SEQUE

RR JOhns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ambertini A.W., Alloni G., Arbertini A.W., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bans A., Braun M., Brignoll S.C., Bron. S., Brotillet S., Eruschi C.V., Caldwell B., Caumony S.C., Eron. S., Brotillet S., Ernschi C.W., Olerero I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Beniata K.D., Errington J., Febret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita T., Fuma S., Galizzi A., Galleron N., Ghims S.Y., Glaser P., Goffeau A., Golighily E.J., Grandi G., Gluseppi G., Guy B.J., Hagen A., Golighily E.J., Grandi G., Gluseppi G., Guy B.J., Hagen K., Halech J., Harendi G., Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Allee S.M., Levine A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medilud N., Mellado R., Mizuro M., Most, D., O'Reilly M., Ogawa K., Ogiwara A., Oudeya B., Park S.H., Portetelle D., Porwollik S., Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Satiochi J., Sekowska A., Serior S.J., Serior P., Shin B.S., Soldo B.,
                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                 93 LETPTVVPVPSMEAHSEAAPTEQT-PVVRQCYHGNGQSYRGTPSTTVTGRTCQSWSSMTP 151
                                                                                                                                                                                                                                                                                            83 RVNCGYPGITSQDCDKKGCCFNDTIPNVVWCYQPIIEAVE-----RDC---SAVEP 130
                                                                                                                                                                                                            42 RTPENYPNAGLTENYC-----RNPDSGKQPWCYTTDPCVRWEYCNLTQCSETESGV 92
                                                                                                                                                                                                                           :::| |:::| |::| |:::| 32 KSRDNCGPPGISPDECVKKGCCFDDSDPDS---IWCYTP----WKFED-TICNPAEPKA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-168 / BGSC1A1;
MEDLINE-95039891; Pubmed-7952181;
Yoshida K.-I., Sano H., Miwa Y., Ogasawara N., Fujita Y.;
"Cloning and nucleotide sequencing of a 15 kb region of the Bacillus subtilis genome containing the iol operon.";
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                           HRHQR--TPENYPNDGLTMNYCRNPDADTGPWCFTTDPSIRWEYCNLTRCS 200
                                                                                                          .) (POTENTIAL).
                                                                                                                                                                               38;
                                                                                                                                                   4.1%; Score 74; DB 1; Length 224;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                       6AE05B3429EFC635 CRC64;
                                                                                                                                                                               70;
      BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         271 AA
                                                                                                                                                                               25; Mismatches
                                                                                                                                                                  38;
                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiology 140:2289-2298(1994).
113
125 152
36 151
6 163
200
200
212
104
24815 MW;
                                                                                                                                                               22.2%;
                                                                                                                                                                               38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                         224 AA;
                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
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135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wippt A., Tamanoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 VPSMEAHSEAAPTEQTPV-----HGNGQSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIME-9603326; Dubmed-7584049;

Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;

**Cloning and sequencing of a 36-kb region of the Bacillus subtilis genome between the gnt and iol operons.";

DNB Res. 2:61-69(4955).

-i- PATHWAY: Myo-inositol catabolism.
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                                                                                                                                                                              Human respiratory syncytial virus (subgroup B / strain 18537).
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FB-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA nēgatīvē-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87289657; PubMed=2441388;
Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 AA; 30770 MW; 4322AE4C18DF21F3 CRC64;
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Search
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 -----GNGQSYRGTFSITVTGR-----TCQSWSSMTPHRHQRTPENYPNDGLTMN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 VPCSICGNNOLCKSICKTIPSNKPKKKPTIKPTNKPTKTINKRDPKTPAKMPKKEIITN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VTLTTVTVQTIKN-----HTEKNI-STYLTQVPPERVNSSKQP---TTSPIHTN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 ISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPWCYITDPCVRWE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 YCRNP-----DADIGPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The G glycoprotein of human respiratory syncytial viruses of subproups A and B: extensive sequence divergence between antigenically related proteins."; proc. Matl. Acad. Sci. U.S.A. 84:5625-5629(1987).

-!- FUNCTION: UNLIEE THE OTHER PARAMYXOVINUS ATACHMENT PROTEINS, THE RESPIRATORY SYNCYTLA VIRUS G PROTEIN LACKS BOTH NEUTRAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 YCNLTQCSETES-----GVLETPTVVPVPSMEAHSEAAPTEQTPVVRQCYH-----
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                                                                                                                                   INFECTED
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                             SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFEC
CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRTONS.
PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 2001;
MEDLINE-98422452; PubMed=9748432;
Nagahashi S., Lussier M., Bussey H.;
"Isolation of Candida glabrata homologs of the Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73.5; DB 1; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 FOTENTIAL.
292 EXTRACELLULAR (POTENTIAL).
81 N-LINKED (GLCNAC. . . ) (PO
86 N-LINKED (GLCNAC. . . ) (PC
100 N-LINKED (GLCNAC. . . ) (PC
32306 MW; BC8C59F69CA7AFCZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                   PIR; B32703; MGNZ18.
InterPro; IPRO0925; Glycoprot_G.
Pfam, PFO0802; Glycoprotein_G; 1
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; M17213; AAA47412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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SEQUENCE FROM N.A.
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completed: September 29, 2003, 08:02:14

time

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 LTENYCRNPDSGKQP--WCYTTDPCVRWEYCNLT--QCSETESGVLETPTVVPVPSMEAH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 -TDGYTIHY-------SPRFKLTGMTGSKLPDTL-LITAPPTPETRVTTG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
                 beta-1,6-glucan synthesis",'
. Bacteriol. 180:5020-5029(1998).
-!- FUNCTION: INVOLVED IN CELL WALL BETA(1->6) GLUCAN SYNTHESIS.
-!- FUNCTION: INVOLVED IN CELL WALL PROBABLY FOUND AT CELL SURFACE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LDQSFDASGGTAKIPIQWLFTPNTPSQDDFTSLTFSLCSG------PNYKIEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 ----SEAAPTEQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 KVIGKLSDIGTIDFEAEVSQSVGANGYYYVQIYAAT----------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 PNDGLTMNYCRNPDADTGPWCFTTDPSIRWEYCNLT--RCSDTEGTVVAPPTV---IQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 SLGPPSEQ---DCMFG--NGKG----YRGKKATTVTGTPCQEWAAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 DIGATIDSKSFDIPYGEQNGKAKFAPMOTOPGTKITAT---TWSRRYATSAVSFFTSLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
cerevisiae KRE9 and KNH1 genes and their involvement in cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100;
                                                                                                                                                                                                                                                                                                                                                                                                              CELL WALL SYNTHESIS PROTEIN KNH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 265; 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 EPHRHSTFIPGINKWAGLEKNYC-RNPDGDINGPWCYTMNPRK 295
                                                                                                                                                                                                                                                                                                                                                                                                                     265 CELL WALL SYNTHESIS PROTE 29046 MW; 6A13BCD6BCOAE2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PTM: O-GLYČOSYLATED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE KRE9 / KNH1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 73; 20.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Cell wall; Signal.
SIGNAL 1 14 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                    EMBL; AF064252; AAC64009.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.13
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      265 AA;
                                                                                                        SIMILARITY)
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055027 mus musculu Q9ukj7 homo sapien Q8ng20 homo sapien Q90675 gallus gall Q9bn9 bos taurus Q9tva8 bos taurus Q9tva8 bos taurus

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Q8NG20
Q90675
Q90675
Q90675
Q90788
Q9065E
Q9065E
Q90613
Q8NCJ9
Q8
                                                                                                                                                                            PRELIMINARY;
[1]
SEQUENCE FROM N.A.
Q9UIR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
 Q9UIR5
                                                                                                   8 ; Search time 36 Seconds
(without alignments)
2207.783 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                            1 KSPVVQDCYHGDGRSYRGIS......TIMNPRKLFDYCDIPLCASS 308
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     830525 segs, 258052604 residues
                                                                                                      September 29, 2003, 08:01:08
                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_bhage:*
    sp_plant:*
    sp_rodent:*
    sp_voints:*
    sp_vertebrate:*
    sp_unclassified:*
                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
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sp_bacteriap:*
sp_archeap:*
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                                                                                                                                                              US-10-088-548-2
1786
                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_23:*
                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                               Perfect score:
                                                                          OM protein
                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                      Run on:
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Q96688 homo sapien Q90488 homo sapien Q90488 homo sapien Q96687 homo sapien Q86462 mus musculu Q13209 homo sapien Q9x70 cyctolagus Q9x77 cyctolagus Q9x77 cyctolagus Q9x77 salmonella Q8203 salmonella Q8671 salmonella Q96710 medicago tr Q6581 homo sapien Q8651 respiratory Q85361 respiratory Q8716 brucella me

Q9cuj3 mus musculu Q9h4c8 homo sapien Q8cdq5 mus musculu Q9supl arabidopsis

ALIGNMENTS

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OGUTES,

DOURS,

DOURS
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Description

B

Query Match Length

Result

SUMMARIES

Q9uir5 homo sapien Q9uir6 homo sapien Q4234 gallus gall G8656 homo sapien Q16609 homo sapien Q01935 homo sapien Q14119 homo sapien Q2811 macaca fasc Q8tcez homo sapien Q9uir8 homo sapien Q9hbM ohmo sapien Q13494 homo sapien Q9umiz homo sapien

Q9UIR5
Q9UIR6
Q9UIR6
Q8A6341
Q8A696
Q16609
Q9UIR7
Q8TCE2
Q9UIR8
Q8TCE2
Q9UIR8
Q9NIB8
Q9NIB8
Q9BSI7
Q9BSI7

335.1 335.5 330.5 300.5

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RESULT 2 Q9UIR6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 DGLIMNYCRNPDADJGPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 QDCMFGNGKGYRGKKATTVTGTPCQEW--AAQEPHRHSTFI--PGTNKWAGLEKNYCRNP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 PENYPNAGLTENYCRNPDSGKQPWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 MEAHSEAAPTEQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PERYPDKGFDDNYCRNPDGKLRPWCYILDPNTPWEFCAIKTC---DVGILNS-----50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 KDLRENYCRNPDGSESPWCFTTDPNIRIGYCS-------QIPKCDVSNE
                                                                            Isokawa K., Yahagi N., Honma J., Tanaka M., Murakami K., Yokoyama H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                    Toda Y.;
The expression of hepatocyte growth factor mRNA is temporally relevant to cardiac endothelial-mesenchymal transformation."; submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: CONTAINS 3 KRINGLE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 550.5; DB 13; Length 215; 40.9%; Pred. No. 4.9e-41; tive 24; Mismatches 81; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Antianglogenic domain of apolipoprotein(a).";
Submitted (JNN-2001) to the EMEL/GenBank/DDBJ databases.
-- SIMILARIYE: CONTAINS 1 KRINGLE DOMAIN.
EMEL; AVO3948; ARX74187.1; --
InterPro; IPR000001; Kringle.
InterPro; IPR000001; Kringle.
Pfam; PR000151; kringle: 1.
Pfam; PR000151; Kringle: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1
NON TER 215 215
SEQUENCE 215 AA; 24949 MW; 55E67AB52DAAF316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2002 (TIEMBLEL. 22, Created)
01-0CT-2002 (TIEMBLEL. 22, Last sequence update)
01-MAR-2003 (TIEMBLEL. 23, Last annotation update)
Antianglogenic AK38 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                             Interpro; IPROGO001; Kringle.
Pfam; PF00051; Kringle; 3.
PRINTS; PRO0018; KRINGLE.
ProDom; PD0001995; Kringle; 3.
SWART; SM00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00021; KRINGLE_1;
PROSITE; PS50070; KRINGLE_2;
                                                                                                                                                                                                        EMBL; D63779; BAA23643.1; -. HSSP; P00747; 1KRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGDINGPWCYTMNP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | :|||||| :|
|DDDSHGPWCYTDDP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match .
Best Local-Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE-Liver;
                                       SEQUENCE FROM N.A.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280
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                                           112 PTEQTPVVRQCYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KSPVVQDCYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNP 60
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XX MEDILNE-21181705; PubMed-11285247;
XA OGOCHACVA W. Kraft H.G., Ehnholm C., Utermann G.;
A OGOCHACVA W., Kraft H.G., Ehnholm C., Utermann G.;
T'single nuclectide polymorphisms in exons of the apo(a) kringles IV
T'ypes 6 to 10 domain affect Lp(a) Plasma concentrations and have
different patterns in Africans and Caucasians.";
Hum. Mol. Genet. 10:815-824(2001).
C. -1- SIMILARITY: CONTAINS! KRINGLE DOMAIN.
REMBL; ART58661, AAF03679.1; JOINED.
REMBL; ART58660; AAF03679.1; JOINED.
REMBL; ART58600; AAF03679.1; JOINED.
REMBL; ART586001 Kringle.
REMBL; REMO051; Kringle.
REMBL; REMO051; Kringle.
REMBL; REMO051; Kringle.
REMDL; REMO051; Kringle.
REMDL; REMO051; Kringle.
REMDL; REMO051; Kringle.
REMDL; REMDL; REMO051; Kringle.
REMDL; REMDL; REMO051; Kringle.
REMDL; REMDL; REMO051; Kringle.
REMDL; REMDCOM, PRO00395; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JAN-1998 (TREMBLrel. 23, Last annotation update)
HGF alpha-chain (Fragment).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Aves; Neognathae; Galliformes; Phasianidae; Galluse;
                                                               1 PIEGIPVYRQCYHGUGGSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                 172 RNPDADIGPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%; Score 634; DB 4; Length 11 100.0%; Pred. No. 9.2e-49; Live 0; Mismatches 0; Indels
    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
12697 MW; 51D4461D9C66312E CRC64;
                                                                                                                                                                                                                                                                                                              01.MAY-2000 (TIENBIREL 13, Created)
01-WAY-2000 (TIENBIREL 13, Last sequence update)
01-WAR-2003 (TIENBIREL 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 AA.
                                                                                                                                                                                                                                                                           113 AA.
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Kringle; Lipoprotein.
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00021; KRINGLE_1; 1. PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein(a) (Fragment). APOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
      Matches 112; Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00130; KR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 1
113 AA;
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NON_TER
SEQUENCE
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RESULT 3

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WEDLINE-21181705; PubMed-11285247;

WEDLINE-21181705; PubMed-11285247;

A GOGGEROCA M., Kraft H.G., Enhabolm C., Utermann G.;

A GOGGEROCA M., Kraft H.G., Enhabolm C., Utermann G.;

Concelloration of polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";

Hum. Mol. Genet. 10:815-824(2001).

C. - SIMILARITY: CONTRINS I KRINGLE DOMAIN.

PERSI, AR158659; AAF03678.1;

C. - SIMILARITY: CONTRINS I.

REBL, AR158659; AAF03678.1;

DR FRIES, PROUGOUS, Kringle: 1.

PRODOM; PROUGOUS; KRINGLE: 1.

PRODOM; PROUGOUS; KRINGLE: 1.

REARY: SWOOD130; KRINGLE: 1.

PROSITE; PSOOU70; KRINGLE: 1.

PROSITE; PSOOU70; KRINGLE: 2;

MIGCOPLOCHED: KRINGLE: 3;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-91200041; PubMed-1826653;
MÄYGZGAVÄ K., Kitamura A., Naka D., Kitamura N.;
"An alternatively processed mRNA generated from human hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DSGKQPWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93087571; PubMed=1280830;
Hartmann G., Naldini L., Weidner K.M., Sachs M., Vigna E.,
Comoglio P.M., Birdmeier W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%; Score 489; DB 4; Length 11 78.0%; Pred. No. 6.5e-36; tive 5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 113 AA; 12815 MW; 4F80ADF8708548CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLRel. 01, Created)
01-NOV-1996 (TrEMBLRel. 01, Last sequence update)
01-NOY-2002 (TrEMBLRel. 20, Last annotation update)
Hepatocyte growth factor, heavy chain precursor.
               01-MAY-2000 (TrEMBirel. 13, Created)
01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-WAR-2003 (TrEMBirel. 23, Last annotation update)
Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 197:15-22(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.4
Best Local Similarity 78.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor gene.
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[1]
SEQUENCE FROM N.A.
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SEQUENCE
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Q02935
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A MEDLINE-55268939; PubMed=7749817;
A MIDLINE-55268939; PubMed=7749817;
Byrne C.D., Schwartz K., Lawn R.M.;
Byrne C.D., Schwartz K., Lawn R.M.;
Toss of a splice donor site at a 'skipped exon' in a gene homologous
to apolipoprotein(a) leads to an mRNA encoding a protein consisting of
a single kringle domain.";
Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
- I Arterioscler. Thromb. Vasc. Biol. 15:65-70(1995).
- SIMILARITY: COWMAINS 1 KRINGLE DOMAIN.
RESP: PO0747; 1PMK.
RESP: PO0747; 1PMK.
RESP: PO0751; kringle.
R PRIME; PRO0051; kringle.
R PRIME; PRO0051; kringle.
R PRIME; SPO0935; Kringle.
R PRIME; SPO0935; Kringle.
R PRAME; SMART; SMO0130; KR: I.L.
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0
                                                                                                                                                                                                                                                               215 VPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 EAAPTEQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VPSLGPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKN 62
                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                             Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Indels
                                                                                                                                                                           Score 544; DB 4; Length 95
Pred. No. 7.1e-41;
1; Mismatches 0; Indels
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PROSITE; PS0001; KRINGLE_2; 1.
Glycoprotein; Kringle.
SEQUENCE 132 AA; 14886 MW; 3794AD30A586DBBA CRC64;
                                                                                                             Glycoprotein; Kringle. SEQUENCE 95 AA; 10553 MW; 31EDC9DB38A372DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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1 Similarity 75.5%; Pred. No. 1.2e-36;
83; Conservative 10; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                    275 YCRNPDGDINGPWCYTMNPRKLFDYCDIPLCAS 307
                                                                                                                                                                                                                                                                                                                                                                        63 YCRNPDGDINGPWCYTMNPRKLFDYCDIPLCAA 95
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PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 1.
SAMAT; SMOGLIO, KR; 1.
PROSITE; PS00071; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                             30.5%;
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01-NOV-1996 (TIEMBIREL 01,
01-MAR-2003 (TIEMBIREL 23,
                                                                                                                                                                         30.55
Best Local Similarity 98.9
Matches 92; Conservative
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Best Local Similarity
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Q9UIR7
ID Q9UIR7
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Matches
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65 Q -- PWCYTIDPCVRWEYCNLIQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQC 122
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

NCBL_TAXID=9541;
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SEQUENCE FROM N.A.
MEDLINE-95395387; PubMed-7666007;
MEDLINE-95395387; PubMed-7666007;
Minton L.L., Newton R.S.;
"Genfibrozil significantly lowers cynomolgus monkey plasma lipoprotein[a]-protein liver apolipoprotein[a] aprotein liver apolipoprotein[a] - frotein liver apolipoprotein[a] mRNA levels.";
J. Lipid Res. 36:1294-1304 (1995).
-i- SIMILARITY: CONTAINS 1 KRINGLE DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 26.7%; Score 477.5; DB 4; Length 296; Similarity 43.2%; Pred. No. 2.1e-34; 86; Conservative 2j; Mismatches 57; Indels 35;
                                                                                                                        | Mastric | Mast
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 AA
                     -i- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
EMBL; M77227; AAA35980.1; -.
HSSP; P14210; 1BHT.
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Science 0:0-0(1991)
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Best Local S
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                                growth factor binds the c-Met receptor and induces cell dissociation but not mitogenesis.',
Proc. Matl. Acad. Sci. U.S.A. 89:11574-11578(1992).
-!- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HERMATONITE CELLS, SEEMS TO BE AN HERMATORYE CELLS, SEEMS TO BE AN HERMATORYE CACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT HAS NO DETECTABLE PROTEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%; Score 481.5; DB 4; Length 290;
43.7%; Pred. No. 9e-35;
tive 21; Mismatches 55; Indels 35; Gaps
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Chan A.M.-L., Rubin J.S., Bottaro D.P., Hirschfield D.W., Chedid M.,
Aaronson S.A.;
   "A functional domain in the heavy chain of scatter factor/hepatocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. HEPATOCYTE GROWTH FACTOR, HEAVY CHAIN.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
Competitive HGF antagonist.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi; Mammalla; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                      HAS NO DELEGIABLE FALLED FALLE
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KRINGLE 2 (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
C8A18A6F0D63200A CRC64;
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272 YTLDPHTRWEYCAIKTC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 FITDPSIRWEYCNLTRC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA; 33765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 43.7% hes 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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       RRITER OF THE STATE OF THE STAT
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112 PTEQIPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLIMNYC 171
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                                                                                                                                                                                                                                                                                                                    PERFORMANCE TROWN N. M. STATE H.G., EDADOLM C., Utermann G.;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-21181059; PubMed-11285247;
MEDLINE-1181059; PubMed-11285247;
MEDLINE-1181059; METICARNA IN REINGLE DOMAIN.
MEDLI ART158655; AAF03677.1; JOINED.
MEDLI ART158656; METINGLE.
MEDLI ART15865690013; KRINGLE.
MEDLI ART158690013; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Enclonetrium;
PISSUB-abclonetrium;
Chen C., Spencer T.E., Bazer F.W.;
"Expression of hepatocyte growth factor and its receptor c-met in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 RNPDADIGPWCFITDPSIRWEYCNLIRCSDIEGTVVAPPIVI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 105
105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ovine uterus.";
Biol. Reprod. 62:1844-1850(2000).
-!- SIMILARITY: CONYAINS 1 KRINGLE DOMAIN.
                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequ
(TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatocyte growth factor (Fragment).
                                                                                                                                                                             Apolipoprotein(a) (Fragment).
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                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                    01-MAY-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9N1B8
                                                  Q9UIR8
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Q9N1B8
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RESULT 11
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                                                                                                                                                                                                                                               65 Q -- PWCYTTDPCVRWEYCNLTQCSETESGVLETPTVVPVPSMEAHSEAAPTEQTPVVRQC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 PSMEAHSE-----AAPTEQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 IRNCIIGKGRSYKGTVSIIKSGIKCQPWSSMIPHEH-----SYRGKDLQENYCRNP-RGE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 YHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                  14 PIME-HKEVVLLLLIFIKSALPEQSHVVQDCYHGDGQSYQGTSSTTVTGRICQAWSSMEP
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                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                    11;
                                                  26.2%; Score 467.5; DB 6; Length 145; 64.7%; Pred. No. 7e-34; iive 11; Mismatches 25; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
L. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
L. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R. Binitaring: CONTAINS 2 KRINGLE DOMAINS.
RMBL; BC022308; AAH22308.1; -.
RIGHTPO: IPRO0001; Kringle.
RIGHTPO: IPRO0304; Pan.
RIGHTPO: IPRO0304; Pan.
RIGHTPO: IPRO0304; Pan.
RPFOWDSI; PAN: 1.
Probom; PD000395; Kringle; 2.
RMART; SM00130; KRINGLE_1; 2.
RMART; SM00130; KRINGLE_1; 2.
RMART; SW00121; KRINGLE_1; 2.
RMART; SW00121; KRINGLE_1; 2.
RMART; PS00021; KRINGLE_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%; Score 466; DB 4; Length 285; 43.1%; Pred. No. 2.1e-33; Live 21; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBIrel. 21, Created)
01-JUN-2002 (TrEMBIrel. 21, Last sequence update)
01-MAR-2003 (TrEMBIREL. 23, Last annotation update)
Similar to hepatocyte growth factor (hepapoletin A, scatter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 AA; 33234 MW; 0A93B073EA86EA61 CRC64;
  OD2DA20A06A5DD87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 AA.
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267 YTLDPHTRWEYCAIKTC 283
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  16097 MW;
                                                                                                                                                                                                                                                                                                                                                                                      133 VTLVPSLEAPSEQ 145
                                                                                                                                                                                                                                                                                                                                                      212 VIQVPSLGPPSEQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 43.1 nes 85; Conservative
                                                                                                    86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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  145 AA;
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Placenta;
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  SEQUENCE
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                                                       Query Match
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Q8TCE2
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                                                                                                    Matches
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Homo sapiens (Human)
                                                                                                Homo sapiens (ASman)
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       SON DER REAL DER REAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 EQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 PDADT-GPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSLGPPSEQDCMFGNGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIANE-27354683; PubMed-12466851;

The FRANTOM CONSORTIUM,

The FANTOM CONSORTIUM,

The RINE Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Malysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

EMBL, 8440840; 5742002).

EMBL, 8440840; 5732020.
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                                                                                                                                                                                                                                                                                                                                                                                     23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus muscúlus (Mouse).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                    ch 14.6%; Score 261.5; DB 6; Length.109; 1 Similarity 39.0%; Pred. No. 9.1e-16; 48; Conservative · 15; Mismatches 37; Indels 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.6%; Score 260; DB 11; Length 209; 44.3%; Pred. No. 2.6e-15; ive 15; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 PDAD-TGPWCFTTDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDNDEOGPWCYTTDPDKRYDYCNIPECEGRGGS-RKPPSVCLSPGI 199
                                                                                                                                                                                                                                                                      109 109
109 Aa; 12501 MW; IF88FE5DBC0D4A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TIEMBLrel. 23, Created)
01-MAR-2003 (TIEMBLrel. 23, Last sequence update)
01-MAR-2003 (TIEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA.
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                            Interpro; TERO00001; Kringle.
Pram: PF00051; Kringle.
PRINTS; PR00018; KRINGLE.
ProDom; P0000395; Kringle; 1.
SWART; SW00130; KR; 1.
PROSITE; PS000121; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
EMBL; AF213397; AAF25945.1; -.
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                             HSSP; P14210; 2HGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 GYR 235
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114 EQTPVVRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMIPHRHQRIPENYPNDGLTMNYCRN 173
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MIDLINE-3186928, PubMed=1832556;

Miyazawa K., Kitamura A., Kitamura N.;

"Structural organization and the transcription initiation site of the "Structural organization and the transcription initiation site of the bunan hepstocyte growth factor gene.";

Biochemistry 30:9170-9176(1991).

-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TayMBLrel. 23, Last annotation update) Hepatocyte growth factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.0%; Score 249.5; DB 4;
Best Local Similarity 47.2%; Pred. No. 2.2e-14;
Matches 42; Conservative 14; Mismatches 32;
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InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR003966; Prothrombin.
Pfam; PF00024; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  EMEL, M75971; AAG53459.1; --
EMEL; M75967; AAG53459.1; JOINED.
EMEL; M75966; AAG53459.1; JOINED.
EMEL; M75968; AAG53459.1; JOINED.
EMEL; M75969; AAG53459.1; JOINED.
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SWART; SM00473; PAN_APP; 1.
PROSITE; PS500021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fram, Frooti, Fox, Parking PRINTS; PRO1505; PROTHROMBIN. PRODOM; PD000395; Kringle; 1.
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NON_TER 208 208
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DR EMBL; 046010; AAC50539.1; -.

DR HSSP: P14210; 1BHT.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003004; Pan.

DR Pfam; PF000024; Pan.

DR Pfam; PF000024; Pan.

DR Probom; PE0000395; Kringle; 1.

DR PROSITE; PS0000139; Kringle; 1.

DR PROSITE; PS000013; KRINGLE_1; 1.

DR PROSITE; PS000013; KRINGLE_2; 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SMART; SW000473; Pan_AP: 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SWART; SW000473; Pan_AP: 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

DR PROSITE; PS00001; KRINGLE_1; 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SWART; SW000473; Pan_AP: 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SWART; SW00473; Pan_AP: 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SWART; SW00473; Pan_AP: 1.

DR PROSITE; PS00001; KRINGLE_2; 1.

SW Glycoprotein; KRINGLE_2; 1.

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September 29, 2003, 08:03:47; search time 82 Seconds (without alignments) 176.148 Million cell updates/sec
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539
1 KSPVYQDCYHGDGRSYRGIS......DPCVRMEYCNLIQCSETESG 91
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 91
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human apolipoprote Human plasminogen Human apolipoprote Plasminogen kringl Human kringle 4. Amino acid sequenc Murine kringle 4. Human OREX protein
SUMMARIES	AAY72945 AAB01909 AAX77720 AAY72946 AAY72946 AAB08414 AAW07550 AAB08414
DB	22 22 21 22 22 22 17 23 23
% Query Match Length DB	1 1 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
% Query Match	100.0 77.0 77.0 74.1 73.7 71.1 71.1 71.1 71.1
Score	539 415 402 402 397 383 377 330 330
Result No.	11084506

Murine kringle 3.	Human kringle 3.	Rhesus kringle 3.	Porcine kringle 3.	Human plasminogen		Bovine kringle 3.	Kringle-1 of plasm	A multifunctional	SEQ ID 113 of W099	EQ ID 113 c	K1 domain of plasm	inogen	lasminog	Rhesus kringle 1.	Plasminogen kringl	plasminog	Bovine kringle 1.	Human plasminogen	Bovine kringle 2.	Porcine kringle 1.	human kringle 1.	Human plasminogen	murine kringle 1.	Porcine kringle 2.	Synthetic N-termin	Human plasminogen	nce encod		Rhesus kringle 2.	plasmi	acid s	acid	live	de #42	Peptide #4326 enco
55	AAW07555	53	AAW07557	AAB01908	AAB08412	S	AAR14661	AAY02110	AAY02134	ന	AAP81360	AAR96221	Ė	AAW07546	AAP93230	AAB01906	AAW07548	AAY77719	AAW07553	AAW07547	AAW07545	AAY58868	AAW07544	AAW07552	AAP90598	AAB01907	AAP94401	AAW07550	AAW07551	AAY77721	1	1	516	3159	
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ALIGNMENTS

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Human; angiogenesis inhibitor; LK6; apolipoprotein(a) kringle domain; angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy; cytostatic, antirheumatic; antiarthritic; antipsoriatic; psoriasis; coultar angiogenic disease; endothelial cell proliferation; tumcour; cell migration.
                                                                                      Human apolipoprotein(a) kringle domain IV36, LK6 protein.
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                                                                                                                                                                                                                                                                                                               Chung
                                                                                                                                                                                                                                                                                          (MOGA-) MOGAM BIOTECHNOLOGY RES INST
                                                                                                                                                                                                                                                                                                               Yum J,
                    AAY72945 standard; Protein; 91 AA.
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                                                                 (first entry)
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N-PSDB; AAD03256.
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                                                                                                                                                                             Homo sapiens.
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                                           AAY72945;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human ik6 protein which contains the amino acid sequence of human apolipoprotein(a) kringle domain IV36 (KIV36). The human apolipoprotein(a) kringle domains IV36 (LK6 protein). IV37 (LK7 protein) and V38 (LK8 protein) together form the angiogenesis inhibitor, KK8 protein. LK68, LK6, LK6, LK7, and LK8 are inhibitors are of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo choricallantoic membrane (CAM). LK68 protein, its single kringles or their functional equivalents, are useful for treating angiogenesis-mediated diseases, such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic disease in animals or humans. LK68 is useful as an anticancer agent and also for inhibiting primary tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KSPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLIENYCRNP
                       Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                     Claim 1; Page 44-45; 50pp; English.
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97US-0832087.
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Matches 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                           diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g. heamargiomas, osler-webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., crohm's disease, atherosclerosis), diseases which have amplogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences Abdol96-Bol99 represent fragments of human plasminogen used in an exemplification of the invention.

Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kringle 4; plasminogen; anti-angiogenic; angiogenesis; angiostatin; cytostatic; antiarthritu; antihneumatic; antidabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; antiarteriosclerotic; human; dermatological; cancer; tumour; birth control; vascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VVQDCYHGDGQSYRGTSSTTTGKKCQSWSSMPPHRAQKTPENYPNAGLIMNYCRNPDAD 60
                                                        The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of anglogenesis and endothelial cell proliferation and migration. The peptides are useful for treating anglogenic diseases, primary and metastratic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopojetic malignancies such as leukaemias and immens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VVQDCYHGDGRSYRGISSTIVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSG 63
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Pred. No. 4.1e-31;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 KQPWCYTTDPCVRWEYCNLTQCSETES 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human plasminogen kringle 4 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Example 17; Page -; 48pp; English.
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RESULT 5
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                                                                                                                                                                        Such diseases include cancers such as solid tumours, blood born tumours such as leukemlas, tumours metastasis, benign tumours such as such as a coustic actionas, used tumours and proper and proper actionas, returning transported arthritis, ocular angiogenic diseases such as diabetic retinopathy, retinopathy of prematurity macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber syndrome, myocardial angiogenesis, plaque neovascularization, telangiectasia, hemophiliae joints, angiofibroma, and wound granulation. The fragments are also useful in treatment of disease of excessive or abnormal stimulation of endothelial cells. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VQDCYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VQDCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADK 60
                                                                                                                                                                                                                                                                                                            diseases include intestinal adhesions, atherosclerosis, scleroderma, and hypertrophic scars. The fragments can be used as birth control agents by preventing vascularization required for embryo transplantation. The present sequence represents the kringle 4 sequence of human plasminogen
                                                                                                                       The invention provides fragments of kringle 1, 2 or 4 of human plasminogen that contain a lyshe binding site and have anti-angiogenic activity. The peptides of the invention function as antianglogenic agents, for the treatment process and diseases involving angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, angiogenesis inhibitor, LK7; apolipoprotein(a) kringle domain; angiogenesis-mediated disease; cancer; rhemmatoid arthritis; therapy; cytostatic; antirhemmatic; antirhemmatic; antipsoriatic; psoriasis; ocular angiogenic disease; endothelial cell proliferation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                            Novel lysine binding fragments angiostatin used as antiangiogenic agents in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, psoriasis, atherosclerotic plaque formation, and other
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 405; DB 21;
Pred. No. 3.2e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 QPWCYTTDPCVRWEYCNLTQCSET 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPWCFTTDPSVRWEYCNLKKCSGT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY72946 standard; Protein; 89 AA.
                                                                                              Disclosure; Fig 3; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      75.1%;
79.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Conservative
                                                                   angiogenesis diseases
WPI; 2000-171200/15.
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200119868-A1.
                                                                                                                                                                                                                                                                                                                                                                   (angiostatin).
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1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 60
                                                                                                                                                                                                                                                                            The present sequence is human LK7 protein which contains the amino acid sequence of human apolipoprotein(a) kringle domain LV37 (KM7). The human apolipoprotein(a) kringle domain LV36 (LK6 protein). IV37 (LK7 protein) and V38 (LK8 protein) 1096ther form the anglogenesis inhibitor, LK68 protein. LK68, LK6, LK7 and LK8 are inhibitors are of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo choricallantoic membrane (CAM). LK68 protein, its single kringles or their functional equivalents, are useful for treating anglogenesis mediated diseases, such as cancer, rheumatoid arthritis, psoriasis or ocular anglogenic also for inhibiting primary tumour growth.
                                                                      Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGK
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Pred. No. 6.5e-30;
8; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen; activator; t-PA; fibrin; kringle domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GPWCFTTDPSIRWEYCNLTRCSDTE
                                                                                                                                                                                                                              Claim 2; Page 45-46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP93231 standard; peptide; 82 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.6%;
77.6%;
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(first entry)
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Best Local Similarity 77.6
Matches 66; Conservative
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N-PSDB; AAN92238.
WPI; 2001-244787/25.
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                        N-PSDB; AAD03257
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03-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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24-FEB-1999;
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18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000.
                                                                                                                                           Query Match
Best Local Si
Matches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB08414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08414
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                           The sequence is encoded by a synthetic oligonucleotide and is the kringle 4 domain of plasminogen. It is used to construct a modified plasminogen activator (mPA) of greater fibrin selectivity than normal PA. The mPA is used in the treatment of pulmonary embolism, thrombosis, myocardial
                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to new methods and compositions for inhibiting endothalial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 2, kringle 1, krin
                                                                                                                                                                                                                                                                                                                                                     4 VVQDCYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSG
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of angiostatin fragments or aggregates - for inhibiting
                                                                                                                                                                                                                                                         Length 82;
                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                         73.7%; Score 397; DB 10; 79.3%; Pred. No. 1.7e-29; tive 7; Mismatches 10;
                                                                                                                                      strokes.
25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cao Y, Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 KGPWCFTIDPSVRWEYCNLKKC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                64 KQPWCYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 116; 203pp; English.
Disclosure; fig 3b; 80pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW07560 standard; protein; 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US05856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0429743.
96US-0605598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0612788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                       65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                             82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human kringle 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9635774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1996;
                                                                                                                                           infarct and
                                                                                                                                                              (Updated on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-1996
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW07560;
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopath; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Gastleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
                                                                                                                                                                                                                                                                                                                                         8 CYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPW
                                                                                                                                                                                                                                                                                                                                                                                                           1 CYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADKGPW
                                                                                                                                                                                                                                                                            Gaps
diagnosis, detection and therapy. human kringle 4, is a specific angiostatin used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                              Length 78;
                                                                                                                                                                                                       Score 383; DB 17; Length 7
Pred. No. 3.2e-28;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of kringle 4 of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chopp M, Wang L, Mikkelsen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FORD-) FORD HEALTH SYSTEM HENRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB08414 standard; Protein; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                          71.18;
79.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0121341.
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99US-0166176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-2000; 2000WO-US04798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                        62; Conservative
                                     ine present sequence,
fragment which can be
          antibodies for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-572016/53.
                                                                                                                                                                                                                                             Similarity
                                                                                                                                         78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200049871-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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CYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQEW 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-2001
                                                                                                                                                                               89
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP02801
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                                                                                                                                                                               5 VQDCYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGK 64
                                                                                                                                                                                                                                      1 VQQCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNNGLTMNYCRNPDADK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine plasminogen. The active component can be used for treating anglogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, murine kringle 4, is a specific angiostatin fragment which can be used in the invention, and represents amino
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
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                                                                                                ö
    Length 83;
                                                                                                Indels
                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim KL;
         DB 21;
         Score 377; DB 21;
Pred. No. 1.2e-27;
                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids 377-454 of murine plasminogen.
                                                                                                                                                                                                                                                                                                                                                              65 QPWCYTTDPCVRWEYCNLTQCS 86
                                                                                                                                                                                                                                                                                                                                                                                                                | |:|||| ||||||| :||
61 GPTCFTTDPSVRWEYCNLKKCS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 115; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW07559 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0429743.
96US-0605598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0612788.
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         69.98;
                                              76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-518662/51.
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                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine kringle 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9635774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW07559;
         Query Match
                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cao I,
                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
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Gaps

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Indels

14;

9; Mismatches

55; Conservative

Matches

Best Local Similarity

Query Match

64.9%; Score 350; DB 17; Length 78; 70.5%; Pred. No. 3.6e-25;

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Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyrodism; cholesterol ester storage disease; immune deficiency; immune disorder; infecticus disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
The present invention describes substantially purified human proteins (referred to as open reading frame, ORRX, where X is 1-11491 (see Table in the specification). ABMI5762 to ABY1252 encode the human ORFX proteins given in ABPD00010 to ABP11500. ORRX proteins are useful for treating or preventing a pathology associated with an OREX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with OREX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, ostecarthrits, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic upupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                      Human ORFX protein sequence SEQ ID NO:5584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID 5584; 1037pp; English
                                                                                                                                                                                                                      ABP02801 standard; Protein; 86 AA
                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-228716P.
                                                                                           CYTTDPSVRWEYCNLKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836.
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                                                                  CYTYDPCVRWEYCNLTQC
                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN18553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000;
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Homo sapiens.
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22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1996;
 angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                    AAW07555;
                                                                                                                                                                                                  89
                                  Seguence
                                                                   Query Match
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                                                                                                   Matches
                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                   1;
                                                                                                                                                                                    1 KSPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNP 60
                                                                                                                                                                                                      N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                   ;;
                                                                                                                Length 86;
                                                                                                                                                   13; Indels
                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Folkman MJ, Lin J, Oreilly MS, Sim KL;
                                                                                                                63.0%; Score 339.5; DB 23
67.5%; Pred. No. 3.7e-24;
ive 13; Mismatches 13;
                                                                                                                                                                                                                                                   61 DSGKQ-PWCYTTDPCVRWEYCNL 82
                                                                                                                                                                                                                                                                    63 DNDQRGPWCFTTDPSVRWEYCNL 85
                                                                                                                                                                                                                                                                                                                                                                    AAW07554 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 111; 203pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS MEDICAL CENT
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95US-0429743.
96US-0605598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-1997 (first entry)
                                                                                                                                  Best Local Similarity 67.59
Matches 56; Conservative
systemic cytokine damage.
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                                                                                   86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine kringle 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-1996;
26-APR-1995;
22-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                   AAW07554;
                                                                                     Sequence
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                    RESULT 10
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67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, human kringle 3, is a specific anglostatin fragment which can be used in the invention, and represents amino
                                                                                                                                                                                                8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGRQPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
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                                                                Length 78;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sim KL
                                 Score 285; Db 17,
No. 3.7e-19;
                                                                                                 Pred. No. 3.7e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acids 178-255 of human angiostatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW07555 standard; protein; 78
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                                                                                                                                                                                                                                                                                                                         CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                               |||||| :||||| : |
61 CYTTDSQLRWEYCEIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0612788.
95US-0429743.
96US-0605598.
                                                                52.9%;
59.0%;
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                                                                                                                            46; Conservative
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                                                                                                 Local Similarity
78 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human kringle 3.
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The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 2, kringle 1, krin
           CYHGDGRSYRGISSTIVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
                                              1 CLKGTGENIRGDVAVIVSGHTCHGWSAQIPHTHNRTPENFPCKNLDENICRNPDGEKAPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CLKGRGENIRGTVSVTASGHTCQRWSAQSPHKHNRTPENFPCKNLEENYCRNPDGETAPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 113-114; 203pp; English.
                                                                                                                                                                                                                                                                                                                        AAW07557 standard; protein; 78 AA.
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96US-0605598.
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                                                                                                                          68 CYTIDPCVRWEYCNLTQC
                                                                                                                                                          61 CYTTNSQVRWEYCKIPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0612788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AA;
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26-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                 RESULT 13
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Kringle 2, kringle 3, kringle 1-3, kringle 1-3, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-4 or Kringle 1 described from a plasminogen and searched from a plasminogen from a plasminogen from a plasminogen from a plasminogen from the sed for treating an independent and diseases such as cencer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, Rhesus kringle 3, is a specific angiostatin
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                                                                                                                                                     1 CLKGTGENYRGNYAVTVSGHTCQHWSAQTPHTHNRTPENFPSKNLDENYCRNPDGKRAPW 60
                                                                                                                    8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLJENYCRNPDSGKQPW 67
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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can be used in the invention, and represents amino
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Pred. No. 8.6e-19;
7; Mismatches 26; Indels
           Length 78;
                                                             24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new methods and compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sim KL;
     Score 281; DB 17;
Pred. No. 8.6e-19;
); Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Pages 112-113; 203pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAW07556 standard; protein; 78 AA.
                                                             10;
                                                                                                                                                                                                                                                                 |:||: |||||| : |
CHTINSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                 68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIL-) CHILDRENS MEDICAL CENT
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57.7%;
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95US-0429743.
96US-0605598.
  52.1%;
56.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                44; Conservative
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Best Local Similarity 57.7
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-518662/51
Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus kringle 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1995;
22-FEB-1996;
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14-NOV-1996.

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68 61

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4 CLKGPGENYRGNNAVIVSGSTCQHWSAQIPHTHNRTPENFPCKNLDENYCRNPDGKRAPW 63
                                4 CLKGTGENYRGNVAVIVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAPW 63
  8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a human polypeptide which is a potent anglogenesis inhibitor, and is designated KED. KED polypeptide, kringle proceins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosolerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory bowel disease, adult respiratory distress syndrome, Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangioma. The present sequence represents kringle 3 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 4.1e-18;
9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasminogen, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of kringle 3 of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chopp M, Wang L, Mikkelsen T;
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                                                                                                      68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                    |:||: |||||| : |
CHTINSOVRWEYCKIPSC 81
                                                                                                                                                                                                                                                                                        AAB08412 standard; Protein; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.8%;
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99US-0121633.
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                  RESULT 15
AAB08412
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastrase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of angiogenesis and endothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, kin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and blymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), coular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber
                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen; human; Kringle domain; endothelial cell proliferation; anglogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antiproliferametory; antiuloer; antirheumatic; antiarthritic; antianglogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Orohn's disease, atherosclerosis), diseases dwhich have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta. Sequences AABO1905-B01919 represent fragments of human plasminogen used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is not shown in the specification, but is derived the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                      Human plasminogen kringle 3 (Thr253-Ser335).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 17; Page -; 48pp; English.
                                                                                                                                                                               AAB01908 standard; Protein; 83 AA
CYTTDPCVRWEYCNLTQC 85
                          CYTTDSEVRWDYCKIPSC 78
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97US-0832087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-349573/30.
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Matches 44; Conserv
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05-MAY-1997;

03-MAY-1996; 03-APR-1997; Davidson DJ;

Homo sapiens

AAB01908;

AAB01908

US6057122-A. 02-MAY-2000 67

Sequence

Query Match

figure 1.

Note: from us-10-088-548-4.sep29.rai

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TYPE: PRT
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Sequence 5, Appli
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Sequence 23,
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539
1 KSPVYQDCYHGDGRSYRGIS......DPCVRWEYCNLTQCSETESG
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
           GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-612-788-23

US-09-066-028-23

US-09-066-028-23

US-09-135-325-23

US-09-135-325-22

US-09-135-325-17

US-09-135-325-17

US-09-135-325-18

US-09-066-028-18

US-09-035-325-18

US-09-035-325-18

US-09-035-325-20

US-09-036-038-21

US-09-036-038-21
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US-08-832-087B-4
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Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 91
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       Sequence
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APPLICANT: Ji, Richard Wei-Dong
APPLICANT: Ji, Richard Wei-Dong
APPLICANT: Ji, Richard Bibling FRAGMENTS OF ANGIOSTATIN
TITLE OF INVENTION: LYGINE BINDING FRAGMENTS OF ANGIOSTATIN
FILE REFERENCE: D811Sequences
CURRENT APPLICATION NUMBER: US/09/348,953
CURRENT FILING DATE: 1999-07-07
PRIOR FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 84
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llarity 79.8%; Pred. No. 1.3e-36;
Conservative 6; Mismatches 11;
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Co'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GPWCFTTDPSVRWEYCNLKKCSGT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09348953 Patent No. 6538103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: human
US-09-348-953-2
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Best Local Simi
Matches 67;
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US-08-612-788-23
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Georgia

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ATTORNEY/AGENT INFORMATION:
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Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-066-028-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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Patent No. 585421
GENERAL INFORMATION:
FAPPLICANT: Cao, Vihia,
APPLICANT: Cao, Vihia,
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STREET: 30303
COUNTRY: US
COUNTRY: US
COUNTRY: US
COUNTRY: US
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.1%; Score 383; DB 2; Length 78; Best Local Similarity 79.5%; Pred. No. 2.9e-34; Matches 62; Conservative 6; Mismatches 10; Indels
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
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APPLICATION WHEBER: US/08/763,528A FLING DATE: 12-DEC-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                  FILLNE UALL:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WATTORNEY/AGENT INFORMATION:
NAME: WATTORNEY/AGENT WIlliam I.
REGISTRATION NUMBER: 36,714
REFERRNCE/DOCKET WOMBER: 05213-0126
TELECHONUTCATION INFORMATION:
TELECHONUTCATION INFORMATION:
TELEFRAX: 404-818-3799
INFORMATION FOR SEG ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
STRANDENESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CFTTDPSVRWEYCNLKKC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                               FILING DATE:
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US-08-763-528A-5
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1 CTHGDGQSYRGISSTTITGKKCQSWSSMTPHRHQKTPENIPNAGLIMNYCRNPDADKGPW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FOLKMEN, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Gao, Yilhai
APPLICANT: San, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF EXQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johose & Askew
SIREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.1%; Score 383; DB 2; Length 78; 79.5%; Pred. No. 2.9e-34; Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
: LOCATION: 1..78
: OTHEN INFORMATION: /note= "Kringle 4 - Figure 3"
05-08-763-5288-5
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NEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/066,028
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CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGBNT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3700
                                                          05940-0251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09066028 Patent No. 6024688
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REPERBNCAPOCKET NUMBER: 0594(
TELECOMMUNICATION INFORMATION:
TELEPRAY: 404-818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conservative
                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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1 CYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRQKTPENYPNAGLTMNYCRNPDADKGPW 60
                                                                                                                                                                                                                                                                                   8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/08612788
Sequence 23, Application US/08612788
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: Gao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OB INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
NORMER OF SEQUENCES: 45
NORMER OF SEQUENCE ADDRESS:
                                                                                                                                                                                                 71.1%; Score 383; DB 4; Length 78; 79.5%; Pred. No. 2.9e-34; tive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DATA PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,714
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPECOMUNICATION INFORMATION:
TELEPECOME: 404-818-3799
                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        68 CYTIDPCVRWEYCNLTQC 85
                 ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                Query Match
Best Local Similarity 79.55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 404-818-3799 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
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FRAGNENT TYPE: N-tern
ORGINAL SOURCE:
ORGANISM: Murine
IMMEDIATE SOURCE:
CLONE: K4
US-08-612-788-22
  HYPOTHETICAL: NO
                                                                                                                          CLONE: K4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CYHGDGQSYRGTSSTTTGKKCQSWSSMTPHRHQKTPENYPNAGLIMNYCRNPDADKGFW 60
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           71.1%; Score 383; DB 3; Length 78; 79.5%; Pred. No. 2.9e-34; Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.

ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
MAKE: WATTEN, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09335325 Patent No. 6521439 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 78 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|||| ||||||| :|
61 CFTIDPSVRWEYCNLKKC 78
23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                               ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                     SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                    62; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 62, Conserva
                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-335-325-23
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US-09-066-028-23
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8 CYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPW 67
                                                                                                                                                              Sequence 22, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: FOLMan, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sin, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
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0
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COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAM:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: GURKNOWN>
PRIOR APPLICATION UNMBER: US/08/612,788
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISSFALION NUMBER: 36,714
REFRERENTION NUMBER: 36,714
REFRERENTION NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.9%; Score 350; DB 4; Length 78 Best Local Similarity 70.5%; Pred. No. 1e-30; Matches 55; Conservative 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-09-335-325-22
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM ITPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTTDPSVRWEYCNLKRC 78
                         68 CYTTDPCVRWEYCNLTQC 85
                                                 61 CYTIDPSVRWEYCNLKRC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: K4
                                                                                                                              RESULT 8
US-09-335-325-22
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                                                                                                        1 CYQSDGQSYRGISSTTITGKKCQSWAAMFPHRHSKTPENFPDAGLEMNYCRNPDGDKGFW 60
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                                                                                     8 CYHGDGRSYRGISSTTVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQPW 67
                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: O'Really, Micheal
APPLICANT: O'Really, Micheal
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
Score 350; DB 2; Length 78;
Pred. No. 1e-30;
9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.9%; Score 350; DB 3; Length 78; 70.5%; Pred. No. 1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY. Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET WUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEFAN: 404-818-3790
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                         1 Similarity 70.5%;
55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.38;
    64.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHEICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Murine
| IMMEDIATE SOURCE:
| CLONE: K4
US-09-066-028-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
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  Query Match
Best Local Similarity
Matches 55; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                          US-09-066-028-22
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1 CLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNPDGETAPW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
FITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%; Score 285; DB 3; Length 78;
59.0%; Pred. No. 1e-23;
tive 6; Mismatches 26; Indels
                                                                                                                                                                                                                                  COMPUTER: LBM Y. Coungellate.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
APPLICATION NUMBER: 08/612,788
FILING DATE:
APPLICATION NUMBER: 36/12,788
FILING DATE:
RETERRANDON NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: A04-818-7700
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STRET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STAME: Georgia
COUNTRY: U.S.
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
                                                                           CITY: Atlanta
STATE: Georgia
CONTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 CYTTDPCVRWEYCNLTQC 85
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61 CYTIDSQLRWEYCEIPSC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 59.08
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Murine
) IMMEDIATE SOURCE:
; CLONE: K3
US-09-066-028-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FOLKMEN, M. Judah
APPLICANT: O'REILLY, Micheal
APPLICANT: Go, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
                                                                                                APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Vilhai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NOMBER OF EXQUENCES: 45
NOMBER OF ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.9%; Score 285; DB 2; Length 78; Best Local Similarity 59.0%; Pred. No. 1e-23; Matches 46; Conservative 6; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                               E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05213-0126
                                   Sequence 17, Application US/08612788 Patent No. 5837682 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
RAME: WATTEN, William L.
REGISTRATION NUMBER: 36,714
REFERRNCEA/COKET NUMBER: 05213
TELECOMMUNICATION INFORMATION:
TELEFRAN: 404-818-3700
TELEFRAN: 404-818-3700
INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-te
ORIGINAL SOURCE:
ORGANISM: Murine
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                                                                                                                                                                                                                                                                               STREET: 191 Peac
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.
ZIP: 30303-1769
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; CLONE: K3
US-08-612-788-17
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US-09-066-028-17
              US-08-612-788-17
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGNENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
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                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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US-08-612-788-18
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Fatent No. 5837682
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
APPLICANT: Sim, B Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.9%; Score 285; DB 4; Length 78; Best Local Similarity 59.0%; Pred. No. 1e-23; Matches 46; Conservative 6; Mismatches 26; Indels
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READSLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325
FILING DATE: 1.7-0n.-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: -Unknown>
APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-018-3799
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: anino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
WOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGNENT TYPE: N-terminal
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
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STATE: Georgia
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US-08-612-788-18
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8 CYHGDGRSYRGISSTIVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQPW 67
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APPLICANT: FOLKMan, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Sim, B. Kim Lee
APPLICANT: Sim, B. Kim Lee
ITILE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 52.1%; Score 281; DB 2; Length 78; Best Local Similarity 56.4%; Pred. No. 2.7e-23; Matches 44; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Jones & Askew
191 Peachtree Street, 37th Floor
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET WUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 and no a cids

LENGTH: 78 and no a cids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08612788 Patent No. 5837682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:||: |||||| : |
61 CHTINSQVRWEYCKIPSC 78
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NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Atlanta
STATE: Georgia
COUTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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67

Gaps

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1 CLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPSKNLDENYCRNPDGKRAPW 60
                                                                                                                                                                                                                                                                                                      8 CYHGDGRSYRGISSTTVIGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPDSGKQPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  52.1%; Score 281; DB 3; Length 78; 56.4%; Pred. No. 2.7e-23; tive 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05213-0126
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
PILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Warren, William L.
REGISCPATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3709
                                                                                                                                                                                                                                                                                                                                                                                                                |:||: |||||| : |
61 CHTINSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                       68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                        HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT HYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rhesus monkey
                                                                                                                                                                                                                                                              44; Conservative
                                                                                                           ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: K3
      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S. ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                           US-09-066-028-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CLKGTGENYRGDVAVIVSGHTCHGKSAQTPHTHNRTPENFPCKNLLDENYCRNPDGEKAPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                 Length 78;
                                                                                                                                                                                                                                                                                                                                                               Score 281; DB 2; Length 78
Pred. No. 2.7e-23;
7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Cacardia
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER: ELOPPY disk
WEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGIERATION UNDERE: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEFAX: 404-618-3700
TELEFAX: 404-818-3799
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PARCOR APPLICATION DATA:
PAPLICATION NUMBER: 08/612,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CYTTNSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 CYTTDPCVRWEYCNLTQC 85
TELEFAX: 404-818-3799
INFORMATION POR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
                                                                                                                                                                                                              FRAGMENT TYPE:

ORIGINAL SOURCE:

OROGNINAL SOURCE:

OROGNINA:

IMMEDIATE SOURCE:

CLONE: K3
US-08-612-788-19
                                                                                                                                                                                                                                                                                                                                                             Query Match 52.1%;
Best Local Similarity 57.7%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-066-028-18
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                                         Query Match 52.1%; Score 281; DB 3; Length 78; Best Local Similarity 57.7%; Pred. No. 2.7e-23; Matches 45; Conservative 7; Mismatches 26; Indels
; CLONE: K3
US-09-066-028-19
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Search completed: September 29, 2003, 08:23:21 Job time : 31 secs

QY g

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September 29, 2003, 08:22:08; search time 63 Seconds (without alignments) 218.555 Million cell updates/sec
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1 KSPVVQDCYHGDGRSYRGIS.....DPCVRWEYCNLIQCSETESG 91
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566894 seqs, 151307093 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                 US-10-088-548-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0 Maximum DB seq length: 91
                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 9, Appli	Sequence 23, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 19, Appl	Sequence 18, Appl	Sequence 19, Appl	Sequence 18, Appl
SUMMARIES	QI 1	US-09-753-064-5	US-09-761-120-23	.0 US-09-335-325-23	.2 US-10-267-137-9						10 US-09-335-325-17				.0 US-09-335-325-19	.5 US-10-131-241-18
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	Query Match Length DB	7	7	7	7	~	7	7	7	7	7	7	7	7	7	78
	Query	1.1	1.1	1.1	71.1	1.1	4.9	4.9	4.9	2.9	5.9	5.9	2.1	2.1	2.1	2.1
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	Score	383	383	383	383	383	350	350	350	285	285	285	281	281	281	281
	Result No.	П	7	ო	4	ស	9	7	œ	σ	10	11	12	13	14	12

SEQUENCE CHARACTERISTICS:

e 19 20, e 20 e 20 e 20	Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 12, Appl Sequence 9, Appli Sequence 9, Appli	724484	A A A	Sequence 8, Appli Sequence 10, Appl Sequence 7, Appli Sequence 7, Appli Sequence 15, Appli
5-10-131-24 5-09-761-120 5-09-335-32 5-10-131-24 -09-753-064 -09-751-120	7 01-120- 9-335-325 0-131-241 0-267-137 761-120- 9-335-325	120- 120- 120- 120- 120- 120-	-241- 064-2 120-8 120-1 120-1 -325- 137-	US-10-131-241-8 US-10-131-241-10 US-09-335-325-7 US-10-131-241-7 US-09-761-120-15
100000	10 12 10 12	16911691	1000012	12 10 12 12 12
7 7 7 8 8 7 7 8 8 7 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 8 7 8 8 8 8 7 8	77777	77777	8 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	000000000000000000000000000000000000000
522 512 512 513 513 513 54 54	0.00.00.44.4 0.00.00.00.00.00.00.00.00.00.00.00.00.0	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
281 278 278 277 277	273 273 273 271 250.5 250.5	2242 2449 2499 2499 2499 2499 2499 2499	247.5 247.5 247.5 247.5 247.5 247.5	
16 17 18 19 20 21	444444	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	<i>wwwwwa</i> 47000000	4 4 4 4 4 1 4 6 4 8

ALIGNMENTS

RESULT 1

US-09-753-064-5

Sequence 5, Application US/09753064

Patent No. USZ0010016644A1

GENERAL INFORMATION:

TILE OF INVENTION: Endothelial cell Proliferation Inhibitor

MUMBER OF SEQUENCES: 6

CORRESSES: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STREET: 191 Peachtree Street, 37th Floor

CONPUTR: Goorgia

COMPUTR: Reabable FORM:

MEDIUM TYPE: Floppy disk

COMPUTR: 1303

COMPUTR: 1303

COMPUTR: 1303

COMPUTR: 1303

COMPUTR: 100 DATE: 29-Dec-2000

CLASSIFICATION NUMBER: US/09/753,064

FILING DATE: 29-Dec-2000

CLASSIFICATION NUMBER: US 08/763,528

FILING DATE: 12-DEC-1996

ATTORNEY AGENT INFORMATION:

REFERENCE IN WILLIAM L.

REFISCRATION INFORMATION:

TELECOMMUNICATION FOR SEGURAL 1709

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   71.1%; Score 383; DB 10; Length 78; 79.5%; Pred. No. 3.8e-34; Live 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10267137
Publication No. US20030148950A1
GENERAL INFORMATION:
APPLICANT: Xin, Li
APPLICANT: Xin, Li
APPLICANT: Gan, Ren-bao
APPLICANT: Xu, Ren
TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
                                                                                                                      ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                      CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 404-818-3700
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
            O'Reilly, Micheal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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Matches 62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-335-325-23
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APPLICANT: O'RELIN, Michael
APPLICANT: O'RELIN, Michael
APPLICANT: O'RELIN, Michael
APPLICANT: O'RELIN, Michael
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT PELLING DATE: 2001-01-16
PRIOR PAPLICATION NUMBER: 09/761,120
CURRENT FILING DATE: 1999-05-11
PRIOR PLILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SEQ ID NOS: 47
SEQ ID NO 23
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                            8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.1%; Score 383; DB 9; Length 78; Best Local Similarity 79.5%; Pred. No. 3.8e-34; Matches 62; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                             LOCATION: 1..78
OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                         Query Match 71.1%; Score 383; DB 9; Length 78; Best Local Similarity 79.5%; Pred. No. 3.8e-34; Matches 62; Conservative 6; Mismatches 10; Indels
LENGTH: 78 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 23, Application US/09761120
; Patent No. US20020037847A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CYTIDECVRWEYCNITQC 85
|:|||| |||||||| :|
61 CFIIDESVRWEYCNIKKC 78
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US-09-761-120-23
                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                             NAME/KEY: Protein
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US-09-761-120-23
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                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                       US-09-753-064-5
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APPLICANT: FOLKMEN, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmi
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: US/09/761,120
CURRENT APPLICATION NUMBER: 09/309,821
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
FRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Version 3.0
SEQ ID NO 22
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW
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Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 350; DB 9; Length 78;
Pred. No. 1.4e-30;
9; Mismatches 14; Indels
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ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEB: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
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REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22, Application US/09335325; Patent No. US20020164717a1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 CYTTDPCVRWEYCNLTQC 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 64.9%;
Best Local Similarity 70.5%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; OTHER INFORMATION: Kringle 4
US-09-761-120-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Murinae gen. sp.
FEATURE:
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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PELLICANT: Forladay, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT APPLICATION NUMBER: US/10/131,241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CYHGDGQSYRGTSSTTTTGKKCQSWSSMIPHRHQKIPENYPNAGIIMNYCRNPDADKGPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CYHGDGQSIRGISSTTTTGKKCQSWSSWTPHRHQKTPENYPNAGLIMNYCRNPDADKGPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.1%; Score 383; DB 15; Length 78; 79.5%; Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Sequence alignment of kringle domains of CTHER INFORMATION: plasminogen and HGF US-10-267-137-9
                                                                                                                                                                                                                                                                                                                                                                                            Length 78;
                                                                                                                                                                                                                                                                                                                                                                                         Score 383; DB 12; Length 7
Pred. No. 3.8e-34;
6; Mismatches 10; Indels
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                             CURRENT APPLICATION NUMBER: US/10/267,137
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/328,329
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 13
SOFTPARE: FastSEQ for Windows Version 4.0
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR PLICATION NUMBER: US 09/416,802
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
PRIOR PELING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 78
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Patent No. US20020037847A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/10131241 Publication No. US20030012792A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 CYTTDPCVRWEYCNLTQC 85
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                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.1%;
Best Local Similarity 79.5%;
Matches 62; Conservative
            FILE REFERENCE: 524282000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 79.55
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-23
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US-10-131-241-23
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US-09-761-120-22
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APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Worleic Acids Encoding Kringle 1-5 Region Fragments of Plasmir
FILE REPERENCE: 05940-0151 (43171-25068)
CURRENT APPLICATION NUMBER: US/09/761,120
CURRENT PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1999-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Version 3.0
ENGTH: 78
LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
O'REALLY, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Applicate and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
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COMPUTER: READABLE FORM:
COMPUTER: IDBW PC compatible
COMPUTER: IDBW PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <a href="https://dox.doi.org/10.10/">CLASSIFICATION: <a href="https://dox.doi.org/">CLASSIFICATION: <a href="https://dox.doi.org/">CLASSIFICATION: <a href="https://dox.doi.org/">CLASSIFICATION: <a href="https://dox.doi.org/">CLASSIFICATION: <a href="https://dox.doi.org/">CLASSIFICATION: <a href="https://dox.doi.org/">CURROWN></a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 52.9%; Score 285; DB 9; Length 78; Best Local Similarity 59.0%; Pred. No. 1.5e-23; Matches 46; Conservative 6; Mismatches 26; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
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SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 CYTIDPCVRWEYCNLTQC 85
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61 CYTTDSQLRWEYCEIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Kringle 3
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
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APPLICANT: Fortier, Anne H.

TITLE OF INVERVION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVERVION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

FILE REFERENCE: 05213-034 43170-271565

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-10-06

PRIOR PILING DATE: 1999-10-06

PRIOR PILING DATE: 1999-05-21

PRIOR PILING DATE: 1998-05-21

FROM RILING DATE: 1998-05-21

FROM RILING DATE: 1998-05-31

SOFTWARE: PRIOR DATE: 1998-05-31

SOFTWARE: PRIOR DATE: 1998-05-31

SOFTWARE: PRIOR OBJECT OF SOFTWARE: US 09/316,805

SOFTWARE: PRIOR OBJECT OF SOFTWARE: US 09/316,805

SOFTWARE: PRIOR DATE: 1998-05-31

FROM RILING DATE: 1998-05-31

SOFTWARE: PRIOR DATE: 1998-05-32

SOFTWARE: PRIOR DATE: 1998-05-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 64.9%; Score 350; DB 10;
Best Local Similarity 70.5%; Pred. No. 1.4e-30;
Matches 55; Conservative 9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                       ; CLONE: K4
; SEQUENCE DESCRIPTION: SEQ ID NO: 22;
US-09-335-325-22
                                TYPE: amino acid
STRANDENESS: CDRANDONSTRANDENESS: CDRANDONT
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANT.*SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: MAINE
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10131241 Publication No. US20030012792A1 GENERAL INFORMATION:
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Patent No. US20020037847A1
GENERAL INFORMATION:
     LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CYTTDPSVRWEYCNLKRC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holaday, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Murinae sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-761-120-17
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US-10-131-241-22
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TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmi FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: 05/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR APPLICATION NUMBER: 09/806,735
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPW 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of UNDERFN OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%; Score 281; DB 9; Length 78; 57.7%; Pred. No. 4e-23; 1ve 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: «UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren, William L. REGISTRATION NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 78 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <URNCOWN>ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CYTTNSQVRWEYCKIPSC 78
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature; OTHER INFORMATION: Kringle 3 US-09-761-120-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
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Matches 45; Conservative
                                                                                                                                                                                                                                                                                                 ORGANISM: Macaca sp.
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                                                                                                                                                                                                                                                                               TYPE: PRT
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Sequence 17, Application US/10131241

Bublication No. US20030012792A1

GENERAL INFORMATION:
APPLICAN: Holaday, John W.
TELE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Requiating Angiogenesis Using Cencer Markers
TITLE OF INVENTION: A010-271565
CURRENT APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR APPLICATION NUMBER: US 60/086,586

PRIOR FILING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 65

SEQ ID NO 17

SEQ ID NO 17

LENGTH: 78
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Pred. No. 1.5e-23;
6; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                    Score 285; DB 10; Length 78;
Pred. No. 1.5e-23;
6; Mismatches 26; Indels
                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-335-325-17
  TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: FOLkman, M. Judah
APPLICANT: O'Reilly, Michael
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61 CYTTDSQLRWEYCEIPSC 78
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59.0%;
                                                                                                                                       FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                  ch 52.9%;
1 Similarity 59.0%;
46; Conservative (
                                                                                                                                                                                   ORGANISM: Murine IMMEDIATE SOURCE:
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Best Local Similarity 59.0
Matches 46; Conservative
                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                  CLONE: K3
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US-10-131-241-17
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US-10-131-241-17
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Best Local S:
Matches 46
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Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: POLINGAN, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                        ch 52.1%; Score 281; DB 10; Length 78;
I Similarity 56.4%; Pred. No. 4e-23;
44; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-7un-1999
CLASSIPICATION: <UNknown>
PRIOR APPLICATION: <UNknown>
APPLICATION: <UNknown>
APPLICATION: <UNknown>
APPLICATION: <UNknown>
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STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
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NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-335-325-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 404-818-3700
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 78 amino acids
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 CYTIDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CHITUSQVRWEYCKIPSC 78
                                                                                     ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                     CLONE: K3
                                                                                                                                 ORIGINAL
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RESULT 15
US-10-131-241-18
Sequence 18
Sequence 18
Sequence 18
Sequence 18
Publication No. US20030012792A1
GENERAL INFORMATION:
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell ProlifITINE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-034, 43170-271565
CURRENT APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SED ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
THENDER OF SED ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CLKGTGENYRGDVAVIVSGHTCHGWSAQTPHTHNRTPENFPCKNLDENYCRNPDGEKAPW 60
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                                                                                                                                                                                                                                                                  Score 281; DB 10; Length 78;
Pred. No. 4e-23;
7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: September 29, 2003, 08:32:03
Job time: 64 secs
                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 19:
ORIGINAL SOURCE:
ORGANISM: Rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 CYTIDPCVRWEYCNLIQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTTHSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 CYTTDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:||: ||||| : |
61 CHTINSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                                                                                 1 Similarity 57.79
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                          IMMEDIATE SOURCE:
                                                                                                                 CLONE: K3
                                                                                                                                                                                       US-09-335-325-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-131-241-18
                                                                                                                                                                                                                                                                  Query Match
Best Local S:
Matches 45
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 29, 2003, 08:12:27 ; Search time 40 Seconds (without alignments) 218.784 Million cell updates/sec Run on:

Title:

US-10-088-548-4 539 1 KSPVVQDCYHGDGRSYRGIS.....DPCVRWEYCNLTQCSETESG Perfect score: Sequence:

91

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

32085 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 91

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database

pir1:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		smin (v chai	oteinase inhibi		BLT14 protein - ba	_	Iq kappa chain V r	short toxin CM-1b	Iq kappa chain - m	unknown protein, 8	ribosomal protein	hypothetical prote	high potential iro	cobrotoxin b - Chi	replication-associ	hypothetical 8K pr	ursc	long neurotoxin 1	protease inhibitor	protein F22G5.16 [Ig kappa chain V r	class II histocomp		kappa-3 neurotoxin	MHC class II histo	sox protein - less	Š	proteinase inhibit	
SUMMARIES	ID	A60140	S20651	T14395	A37910	S16161	S26459	S29587	T2NJBE	S24216	D96636	G69136	D85557	IHER2	JC5892	PS0142	Q3ECFS	IPDK	N2EP1V	S30578	E86209	S78488	PL0129	I68555	B60549	S38704	S34330	N1NJ3M	B84433	3408
	83	7	7	7	7	7	~	7	r-1	7	~	7	7	Н	7	7	Н	Н	-1	~	7	(7	~	N	7	7	7	Н	N	7
	Length DB	89	86	77	86	88	86	86	57	67	55	88	72	76	82	84	72	81	72	77	84	86	89	88	87	8	52	62	77	86
dł	Query							10.2																						
	Score	329		7		'n.		52		52.5	÷	51	20	S	ď		40	4	φ.	•	œ.	φ.	ω.	٠	48	4	٠	7	7	•
	Result No.	1	7	e	4	5	9	7	ω	σ	10	11	12	13	14	15	16	17	. 18	19	20	21	22	23	24	.25	26	27	28	29

Ig kappa chain V r	Ig kappa chain V r	Iq kappa chain V r	Ig kappa chain V r		short neurotoxin b	spike glycoprotein	spike glycoprotein	hypothetical prote	transcription requ	Ig kappa chain Vr	Ig kappa chain V r	proteinase inhibit	intestinal trefoil	short neurotoxin 2	hypothetical prote
S34084	S34083	S21528	S21522	E58892	G25866	PQ0342	PQ0340	T32946	AD1043	S16842	S16841	C84433	A41441	NIRIZ	T34687
2	~	7	~	7	7	~	7	~	7	N	~	7	7	Н	7
87	87	88	88	55	62	99	99	70	73	87	87	77	81	61	92
•	8.8	•	•	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7		8.6		•
47.5	47.5	47.5	47.5	47	47	47	47	47	47	47	47	46.5	46.5	46	46
30	31	32	33	34	35		37	38		40	41	42	43	44	45

ALIGNMENTS

```
plasmin (EC 3.4.21.7) precursor - chicken (fragment)
```

N,Alternate names: plasminogen C;Species: Gallus gallus (chicken) C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999

Cincossion: A60140
BiSyenes, M.; Patthy, L.
Bischin, Biophys. Acta 832, 326-330, 1985
A;Title: The Kringle 4 domain of chicken plasminogen.
A;Reference number: A60140; MUID:86077796; PMID:4074753
A;Accession: A60140
A;Accession: A60140
A;Molecule type: protein
A;Residues: 1-89 cgrs.
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homo
C;Superfamily: plasmin; kringle homology kRRSC;Superfamily: kringle homology kRRSF;6-83/Domain: kringle homology kRRSF;6-83,77-66,55-78/Disulfide bonds: #status predicted
F;39/Binding site: carbohydrate (Asn) (covalent) #status experimental

Gaps 0; DB 2; Length 89; Query Match 61.0%; Score 329; DB 2; Length 89 Best Local Similarity 61.0%; Pred. No. 2e-25; Matches 50; Conservative 16; Mismatches 16; Indels

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65 6 QDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQ 셤 ŏ

66 PWCYTTDPCVRWEYCNLTQCSE 87 64 PWCYTIDPSVRWEYCNIKRCSD 85 g

δŽ

RESULT 2 S20651

A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-86 < LOS>
A; Residues: 1-86 < LOS>
A; Residues: 1-86 < LOS>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

Query Match

DB 2; Length 86; Score 66; 12.2%;

Gaps

1;

a

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RESULT 6
S26459
Ig Asppa chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Accession: S26459
R; Kayaler, J.
submitted to the EMBL Data Library, April 1991
A; Reference number: S26459
A; Accession: S26459
A; Accession: S26459
A; Accession: S26459
A; Accession: S26459
A; Cross-references: EMBLX59087; NID:q52197; PIDN:CAA41813.1; PID:q52198
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Dunn, M.A.; Highes, M.A.; Pearce, R.S.; Jack, P.L.
J. Exp. Bot. 41, 1405-1413, 1990
J. Exp. Bot. 42, 1405-1413, 1990
A.Fitle: Wolecular characterization of a barley gene induced by cold treatment. A; Reference number: S16161
A.Recession: S16161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GREREGCSDTRC---RCORW-----RRRLOGFGLAAAGGNRYRNKHHYRPAGGDPW- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Hordeum vuîgare (barley)
C:Date: 19-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
C;Accession: S16161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNP----DSGKQPWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                        24 VTGRICQSWSSM-IPHWHQRIPENYPNAGLIENYCRNPDSGKQPWCYTTDPC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TITCSVSSSISSSNLHWYQQKSETSP-------KPWIYGT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 88;
                                                                                                                                                                                                      Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 IVIGRICQSWSSMIPHWHQRIPENYPNAGLTENYCRNPDSGKQPWCYIT
   A,Molecule type: protein
A,Residues: 22-27,29-86 <SEG>
C,Superfamily: snake toxin
C;Keywords: toxin; venom
F;1-21,Domain: signal sequence #status predicted <SIG>
F;22-86/Product: muscarinic toxin 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X57554; NID: 918937; PID: 918938
                                                                                                                                                                                                Score 55.5; DB 2;
Pred. No. 1.1e+02;
5; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.3%; Score 55.5; DB 2; Best Local Similarity 29.4%; Pred. No. 1.1e+02: Matches 20; Conservative 4; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.2%; Score 55; DB 2; I
28.6%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                   Query Match 10.3%;
Best Local Similarity 28.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 --- DPCYR 74
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLT14 protein - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-88 <DUN>
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S29587
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N;Alternate names: MTX2
C;Species. Denforacapis angusticeps (eastern green mamba)
C;Date: 31-7an-1992 #sequence_revision 31-7an-1992 #text_change 17-Mar-2000
R;Ducancel, F; Rowan, B.G.; Cassar, B.; Harvey, A.L.; Menez, A.; Boulain, J.C.
Toxicon 29, 516-520, 1991
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-86 <DUC>
A;Cross-references: GB:X52292; NID:g62765; PIDN:CAA36541.1; PID:g62766
R;Xalte: Risinger, C.; Jołkkonen, M.; Mernstedt, C.; Adem, A.
Foxicon 29, 521-526, 1991
A;Title: Amino acid sequence of a snake venom toxin that binds to the muscarinic acetylc
A;Accession: A37911
A;Status: preliminary
A;Molecule type: protein
A;Residues: Xf. 23-86 <AAR>
A;Reference number: A37911; MUID:91320366; PMID:1862525
A;Attle: A particularly labile Asp-Pro bond in the green mamba muscarinic toxin MTX2. Ef
A;Reference number: S66418; MUID:93402203; PMID:7672121
A;Reference number: S66418; MUID:93402203; PMID:7672121
                                                                                                                                                                                                                                                                                                                                                                                                proteinase inhibitor II - turnip
C;Species: Brassica rapa (turnip)
C;Species: Lo-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T14395
R;Kim, J.B.; Kim, H.U.; Yun, C.H.; Park, B.S.; Cho, W.S.; Ryu, J.C.; Chung, T.Y.
submitted to the RMBL Data Library, March 1996
A; Description: Nucleotide sequences of protease inhibitor II in chinese cabbage.
A;Reference number: Z18029
A; Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T14395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-77 <KIM>
A;Cross-references: EMBL:L31937; NID:g1209257; PID:g1209258
A;Experimental source: unopened flower bud
C;Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ñ
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                                                                                           1 KSPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNP 60
                                                                                                                             18 GISSTIVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPD-----SGKQPWCYTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Gaps
                                 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 57.5; DB 2; Length 7 ilarity 31.7%; Pred. No. 63; Conservative 5; Mismatches 25; Indels
                                 22; Indels
25.4%; Pred. No. 10;
tive 7; Mismatches
                              18; Conservative
                                                                                                                                                                                                         61 DSGKQPWCYTT 71
                                                                                                                                                                                                                                                                -----WIYTT 52
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Best Local Similarity
Matches 20; Conserv
   Best Local Similarity
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Gaps

16; 71

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C. Accession: D96636

R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Dankins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.H.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall A; Title: Sequence and analysis of chronosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal protein L34 - Methanobacterium thermoautotrophicum (strain Delta H)
N;Alternate names: eukaryotic ribosomal protein L34; prokaryotic ribosomal protein I
C;Species: Methanobacterium thermoautotrophicum
C;Date: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change l3-Aug-1999
C;Accession: G69136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani Yi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE000796; GB:AE000666; NID:g2621057; PIDN:AAB84538.1; PID:g26
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
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                                                                                                                                                                                     unknown protein, 87272-87105 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 IVTGRICQSWSSMIPHWHQRIPENYP------NAGLIENYCRNPDSGKQPWCYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 55;
                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 2; Length 85;
Pred. No. 3.1e+02;
               26 GSGTSY----SLIISRMEAEDAATYYCQQWSSYPPHYRCWDQAGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.5; DB 2;
Pred. No. 1.8e+02;
7; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
C;Superfamily: gamma-thionin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-55 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 TDPC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 TRPC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: D96636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: T7P1.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Aate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Aate: 19-Feb-1094 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: S24216
R; Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A; Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excis A; Reference number: S24214; MUID:91217618; PMID:1902500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Joubert, F.J.; Taljaard, N.
Toxicon 18, 191-198, 1980
A;Title: The complete primary structure of toxin CM-1b from Hemachatus haemachatus (ring A;Reference number: A01673; MUID:80236878; PMID:7394807
A;Accession: A01673
                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-86 < KAV>
A; Tossidues: 1-86 < KAV>
C; Yoross-references: EMBL:X59090; NID:952219; PIDN:CAA41816.1; PID:952220; EMBL:X59089;
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S29587; S29586
R;Kavaler, J.
Submitted to the EMBL Data Library, April 1991
A;Recession: S29587
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        short toxin CM-1b - ringhals
C;Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C;Date: 31-Jul-1980 #sequence_revision 31-Jul-1980 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ICQPEQKFC---YSDIWIFFPNHPVYLSGCI--FCRIDESGER--CCTIDRC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 ICOSWSSMIPHWHQRIPENYPN----AGLIENYCRNPDSGKQPWCYTIDPC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 TVTGRTCQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 57;
Pred. No. 1e+02;
7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 2; Length 86;
Pred. No. 1.2e+02;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 1-57 <JOUS
C; Superfamily: snake toxin
C; Keywords: toxin; venom
F;3-19,12-37,40-49,50-55/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.5; DB 2;
Pred. No. 1.7e+02;
2; Mismatches 13;
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A,Molecule type: DNA
A,Residues: 1-67 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%;
28.6%;
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Best Local Similarity 32.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.8
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserv
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SQTPTTKTCSGETNCYKKWWSDHRGT-----IIERGCGCPKVKPGVNLNCCTTDRC 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replication-associated protein - sugarcane streak virus (fragment)
C;Species: sugarcane streak virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CYHGDGRSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLIENYCRNPDSGKQ 65
A,Accession: JC5892
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-82 - CMA
A;Cross-references: GB:Y13399; NID:95419941; PIDN:CAA73829.2; PID:95419942
A;Experimental source: venom
C;Genetics:
A;Introns: 19/1; 54/1
C;Superfamily: snake toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 SSTTVTGRICQSWSSMIPHW---HQRIPENYPNAGLIENYCRNP--DSGKQPWCYTIDPC
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Pred. No. 4.2e+02;
4; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                   9.2%; Score 49.5; DB 2; Length 82; 30.0%; Pred. No. 4.1e+02; rative 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: tomato golden mosaic virus ALl protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: September 29, 2003, 08:22:46 Job time: 43 secs
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Local Similarity 27.6%;
les 16; Conservative 4
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Best Local Similarity 30.09
Matches 18; Conservative
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A; Residues: 1-84 <RYB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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A; Molecule type: protein
A; Residues: 1-76 < TED>
C; Comment: The high potential iron-sulfur protein (HiPIP) are a class of high-redox-pote
d in some other photosynthetic bacteria and in at least one genus (Paracoccus) of haloph
two HiPIP forms are found.
C; Superfamily: high potential iron-sulfur protein
C; Reywords: 4Fe-45; electron transfer; iron-sulfur protein; metalloprotein
F; 38, 41, 54, 70/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cobrotoxin b - Chinese cobra
C;Species: Naja naja atra (Chinese cobra)
C;Species: Naja naja atra (Chinese cobra)
C;Sate: 18-Nar-1998 #sequence_revision 18-Nar-1998 #text_change 21-Jul-2000
C;Accession: JC5892
R;Chang, L.S.; Chou, Y.C.; Lin, S.R.; Wu, B.N.; Lin, J.; Hong, E.; Sun, Y.J.; Hsiao, C.L
J; Bacchen, 122, 1222, 1397
A;Title: A novel neurotoxin, cobrotoxin b, from Naja naja atra (Taiwan cobra) venom: Pur A;Reference number: JC5892; MJID:98158338; PMID:9498573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: A00271
R; Tedro, S.M.; Meyer, T.E.; Kanen, M.D.
Arch. Blochem. Biophys. 241, 656-664, 1985
A; Title: Anino acid sequence of high-redox potential ferrodoxin (HiPIP) isozymes from the A; Reference number: A90077; MUID:85305760; PMID:4037807
                                                                                                                                                                                                                  Pypothetical protein 20726 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9 C; Species: Escherichia coli (species: Internationali (species: Internat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: D85557
A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rosidues: 1-72 <STO>
A;Cross-references: GB:AE005174; NID:g12513475; PIDN:AAG54920.1; GSPDB:GN00145; UMGP:207
A;Experimental source: strain O157:ff7, substrain EDL933
C;Genetics:
A;Gene: 20726
C;Superfamily: Escherichia coli hypothetical 8K protein (fes 3' region)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high potential iron-sulfur protein II - Ectothiorhodospira halophila N;Alternate names: high-redox-potential ferredoxin 2; HiPIP C;Species: Ectothiorhodospira halophila
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             9 RSYKRIPKKTPGGRT-----VTHYRKKPSKHVCAG-----CGKPLHG 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%; Score 50; DB 2; Length 72; 40.0%; Pred. No. 3.2e+02; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| | : || 148 SCQQWLEV--HWRTLTPANF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 TCQSWSSMIPHWHQRTPENY 47
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Best Local Similarity
Matches 8; Conserva
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SEQUENCE OF 22-86.
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RESULT 1
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                                                                                               September 29, 2003, 08:04:12; Search time 23 Seconds (without alignments) 186.062 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                   91
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1 KSPVVQDCYHGDGRSYRGIS.....DPCVRWEYCNLTQCSETESG
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P80958
P18393
P01333
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Q39182
P15817
P01432
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          127863 segs, 47026705 residues
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ATP8_LATCH
NXSB_LATLA
TX48_DENJA
THG3_ARATH
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CXH_HEMHA
NXL2_DENVI
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NXS1_BUNFA
R37A_SULSO
NXS1_PSETE
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HP12_ECTHA
CBTB_NAJAT
YBDZ_ECOLI
INS_ANAPL
NXL1_DENVI
THG1_ARATH
NXL3_BUNMU
NXS3_NAJMO
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CBLE_VISAL
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Maximum Match 100%
Listing first 45 summaries
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                                                                       using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Maximum DB seq length: 91
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46
45.5
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corynebacte

pos taurus bos taurus

P37359 1 Q02376 1 Q8ns15

NIKM_BOVIN RL28_CORGL

MT3_BOVIN

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        Q9xz13 conus texti

Q9xz13 conus texti

G6584 homo sapien

Q56029 salmonella

Q56029 salmonella

P01420 naja haje a

P01421 naja haje a

P56609 tityus bahi

P56609 tityus bahi

P58144 tityus serr

P01388 naja malamo

P49269 aptostichus
 pseudonaja
                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Muscarinic toxin 2 precursor.
Dendroaspis angusticeps (Eastern green mamba).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosaurias Squamata; Scleroglossa; Serpentes; Colubroidea;
NCBL_TaxID-8618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ducancel F., Rowan E.G., Cassar E., Harvey A.L., Menez A., Boulain J.-C.; Sequence of a muscarinic toxin deduced from the cDNA mincleofide sequence ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJURE-513201366; PubMed=1862525;
Karlsson E., Risinger C., Jolkkonen M., Wernstedt C., Adem A.;
*Amino acid sequence of a snake venom toxin that binds to the
muscarinic acetylcholine receptor.";
Toxicon 29:521-526(1991).
-!- FUNCTION: BINDS TO THE MUSCARINIC ACETYLCHOLINE RECEPTOR.
Q9w7k0
P36985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i-SUBERLIUTAR LOCATION: Secreted.
-i-fissur SPECIFICITY: Expressed by the venom gland.
-i-SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSCARINIC TOXIN 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                               86 AA.
                                                                                                                                                                                                           ALIGNMENTS
                                                        EDDF_HUMAN
PAGD_SALTY
NXS3_NAJHA
NXS4_NAJHA
SCX2_TITEA
SCX2_TITEA
NXL2_NAJME
TXP4_APTSC
                             CONTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P01382; INFN.
InterPor, IPR001572; Cytotoxin.
InterPor, IPR001571; Snake_toxin.
Pfam; PF001087; toxin, 1.
PRINTS; PR00282; CYTOTOXIN.
ProDom; PD0001206; Snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
TOXIN; Neurotoxin; 21gnal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
TISSUE=Yenom gland;
MEDLINE=91320365; PubMed=1862524;
                                           NODI DEDDE DE PAGD NXS3 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X52292; CAA36541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    loxicon 29:516-520(1991).
21
86
45
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DISULFID
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toxin CM-1b.
                                                                                                                 NCBI_TaxID=8626;
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12
50
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                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Bukaryoris, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment.";
J. Exp. Bot. 41:1405-1413(1990).
J. Exp. Bot. 40:016 stress.
-!- INDCTION: By cold stress.
-!- MISCELARROUGS: CONTAINS SEVERAL ARGININE RESIDUES IN CLOSE
-!- PROXIMITY WHICH MAY BE INVOLVED IN PROTEIN RNA INTERACTIONS.
                                                                                                                                                                                                                                                84
                                                                                                                                                                                                      24 VTGRICQSWSSM-IPHWHQRIPENYPNAGLIENYCRNPDSGKQPWCYTTDPC 74
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                                                                                                                                                                                                                                                33 VITEDCPAGONVCFKRWHYVTPKNYDIIKGCAATCPKVDNNDPIRCCGTDKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAIN-ov. Igri; TISSUE-Shoot meristen;
Dunn M.A., Hughes M.A., Pearce R.S., Jack P.L.;
"Molecular characterization of a barley gene induced by cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55.5; DB 1; Length 88;
Pred. No. 28;
4; Mismatches 25; Indels
                                                                                                                 Length 86;
                                                                                                                                                         31; Indels
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
6F062C970074D653 CRC64;
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C125D831E9BB40D0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cold-regulated protein BL714.
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                                                                                                                                                                                                                                                                                                                                                               88 AA.
                                                                                                              Score 55.5;
Pred. No. 27;
                                                                                                                                                           5; Mismatches
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(Rel. 41, Last anno
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88 AA; 9796 MW;
63
78
84
9375 MW;
                                                                                                              10.3%;
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Best Local Similarity 29.4
Matches 20; Conservative
                                                                                                                                                           15; Conservative
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                                                                                                                                      Similarity
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21-JUL-1986 (
28-FEB-2003 (
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P26154;
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                     DISULFID
                                                                    SEQUENCE
DISULFID
                                                                                                                 Query Match
                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                   RESULT 2
CR14_HORVU
                                                                                                                                                           Matches
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Gong N.L., Armugam A., Jeyaseelan K.;
"Molecular cloning, characterization and evolution of the genes
encoding a new group of short-chain alpha-neurotoxins in an Australian
elapid, Pseudonaja textilis.";
FEBS Lett. 473:303-310(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gong N.L., Armugam A., Jeyaseelan K.; "Postsynptic Short-chain neurofoxins from Pseudonaja textilis: cDNA cloning, expression and protein characterization."; Eur. J. Biochem. 265:982-989(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudonaja textilis (Eastern brown snake).
Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Blapidae; Acanthophiinae; Pseudonaja.
Hemachatus haemachatus (Ringhals) (Sepedon haemachatus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Hemachatus.
                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: Expressed by the venom gland.
-:- MISCELLANBOUS: LD(50) IS 11.7 MG/KG BY INTRAVENOUS INJECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 TCQSWSSMIPHWHQRTPENYPN----AGLIENYCRNPDSGKQPWCYTTDPC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                       Joubert F.J., Taljaard N.;
The complete primary structure of toxin CM-1b from Hemachatus haemachatus (Ringhals) snake venom.";
Toxicon 18:191-198(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 1; Length 57; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
63DIC7818A8B2E20 CRC64;
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                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: Belongs to the snake toxin family. PIR; A01673; T2NJBE. HSSP; P01382; 1NTN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND IDENTIFICATION OF INTRONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Short neurotoxin 6 precursor (Alpha neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003571; Snake_toxin.
Prefan; Pr90087; toxin; 1.
ProDom; PD000206; snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom gland;
MEDLINE=99449602; PubMed=10518793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom gland;
MEDLINE=20279909; PubMed=10818230;
                                                                                                                                                      TISSUE=Venom;
MEDLINE=80236878; PubMed=7394807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AA;
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4;

m

5

Gaps

12; 63

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
    There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANBOUS: IN E.HALOPHILA, TWO HIPIP ISOZYMES ARE FOUND; THEY HAVE THE LOWEST REDOX POTENTIALS YET DETERMINED.
-!- SIMILARITY: BELONGS TO THE HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tedro S.M., Mayor T.E., Kamen M.D.;
Tedro S.M., Mayor T.E., Kamen M.D.;
Tedro S.M., Mayor T.E., Kamen M.D.;
Isozymes from the extremely halophilic purple phototrophic bacterium,
Ectorhiorhodospira halophila.";
Arch Biolochem. Biophys. 241:656-664(1985).
I-FUNCTION: SPECIFIC CLASS OF HIGH-REDOX-POTENTIAL 4FE-4S
FERREDOXINS. FUNCTIONS IN ANAEROBIC ELECTRON TRANSPORT IN MOST
PURPLE AND IN SOME OTHER PHOTOSYMPHETIC BACTERIA AND IN AT LEAST
ONE GENUS (PARACOCCUS) OF HALOPHILIC, DENITHEFYING BACTERIA.
THE MIDPOINT REDOX POTENTIAL FOR THIS PROTEIN IS +50 MV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
High potential iron-sulfur protein isozyme II (HiPIP 2) (High-redox-potential ferredoxin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 RSYKRIFKKTPGGRT-----VTHYRKKFSKHVCAG-----CGKPLHG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammaproteobacteria; Chromatiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 RSYRGISSTIVIGRICQSWSSMIPHWHQRIPENYPNAGLTENYCRNPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 76;
                                                                                                                                                                                                                                                                                                                                                                                        Length 88;
                                                                                                                                                                                                                                                                                                                                             3F6C1AC5D2E41ECE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12D1524EB0BAF7AC CRC64;
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IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
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Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 1
Pred. No. 82;
6; Mismatches
                                                                                                                                                                          HAMAP; MF_00349; -; 1.
InterPro: IPR001284; Ribosomal_L34E.
Pfan; PP01199; Ribosomal_L34e; 1.
PRINTS; PR01250; RIBOSOMALL34.
ProDom; PD005148; Ribosomal_L34E_C; 1.
PROSITE; PS01145; RIBOSOMAL_L34E; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 88 AA; 10301 WW; 3F6C1AC5D2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transport; Iron-sulfur; 4Fe-4S.
    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Broteobacteria; Gammaproteobz
Ectothiorhodospiraceae; Halorhodospira.
NCBL_raxID=1053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000170; Hipot_ironsulf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85305760; PubMed=4037807;
                                                                                                                                                                                                                                                                                                                                                                                                                                     . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1987 (Rel. 04, Created)
                                                                                                                                      EMBL; AE000796; AAB84538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIPIPERDOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                          9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
8560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity 30.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00374; HIPIPER; PS00596; HIPIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01355; HIPIP;
                                                                                                                                                            G69136; G69136
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P04168; 2HIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPI2_ECTHA P04169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A0027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPI2_ECTHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRGISSTIVTGRICQSWSSMIPH----WHQRIPENYPNAGLIENYCRNPDSGKQPWCYTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Gook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Wang IN., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 YKSLSGTVV----CK-----PHETICYRRIPATHGNAIIDRGCSISCPGGNRPVCCST
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EMBL; AF004973; AAF7524.1; -.

DR HSSP; PO146; INRA.

DR HSSP; PO10026; Snake_toxin.

DR PRODIE; PS000272; Snake_toxin.

DR PRODIE; PS000272; Snake_toxin.

DR PROSIE; PS000272; Snake_toxin.

TOXIN; Mourotoxin; Postsynaptic neurotoxin;

KW Acetylcholine receptor inhibitox; Signal; Multigene family.

SIGNAL

TOX AND SHORT TY.

TO 24 41 BY SIMILARITY.

BY SIMILARITY.

TO 24 79 BY SIMILARITY.

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TO 35; Inc.

TO 35; Inc.

TO 36; Inc.
-i- SUBCELLULAR LOCATION: Secreted (By similarity).
-i- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
-i- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 36, Last sequence update)
50s ribosomal protein L34e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Delta H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
28-FEB-2003 (Rel. 41, Last anno
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DLC 77
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O26137;
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11; Indels

6; Mismatches

Conservative

Matches

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Escherichia coli
                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                                                       01-NOV-1990
                                                                                                                                          01-NOV-1990
16-OCT-2001
                                                                             YBDZ_ECOLI
P18393;
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INS_ANAPL
                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSQIPTIKICSGEINCYKKWWSDARGI------IIERGCGCPKVKPGVNLNCCTIDRC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., SEQUENCE OF 22-82, AND FUNCTION.
TISSUE-Liver, and Venom;
MEDLINE-98158338; PubMed-9498573;
Chang L.-S., Chou Y.-C., Lin S.-R., Wu B.-N., Lin J., Hong E.,
Sun Y.-J., Hsiao C.-D.;
A novel neurotoxin, cobrotoxin b, from Naja naja atra (Taiwan cobra)
venom: purification, characterization, and gene organization.";
J. Biochem. 122:1252-1259(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Indels 13; Gaps
                                                                41 CQFWVDYVNGW-------GYCQHPD------FIDVLVRGEGWCSV 72
                                    29 CQSWSSMIPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYTTDPCVRWE-YCNL 82
                                                                                                                                                                             CBRE_NAJAI STANDARD; PRT; 82 AA.
P80958; 042285;
01.NOY-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cobrotoxin b precursor (CBT b) (Short neurotoxin).
Naja atra (Chinese cobra)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Naja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49.5; DB 1; Length 82;
Pred. No. 1.1e+02;
5; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1FFA21189C08B6E8 CRC64;
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EMBL; AF031472; AAB86636.1; -.
PIR; JCS892; UCS892.
INCRPPO; PO1427; INOR.
InterPro; IPR003571; Snake_toxin.
Propom; PR00087; toxin; 1.
Propom; PS00205; Snake_toxin; 1.
PROSTIE; PS00272; SNAKE_TOXIN; 1.
IOXID: Neurotoxin; PS$19991; PS$19991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COBROTOXIN B.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A., AND REVISION TO 67. IISSUE-Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%;
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Best Local S
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between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-89066678; PubMed-2974033; Pettis G.S., Brickman T.J., McIntosh M.A.; Pettis G.S., Brickman T.J., McIntosh M.A.; "Transcriptional mapping and nucleotide sequence of the Escherichia coli fepA-fes enterobactin region. Identification of a unique iron-regulated bidirectional promoter."; J. Biol. Chem. 263:18857-18863(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rusnak F., Sakaitani M., Drueckhammer D., Reichert J., Walsh C.T.; "Blosynthesis of the Escherichia coli siderophore enterobactin: sequence of the entr gene, expression and purification of Bntr, and analysis of covalent phosphopantetheine."; Biochemistry 30:2916-2927(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SERALN-FL2 / MG1655;
MEDLINE-9745617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1- FUNCTION: COULD BE INVOLVED IN ENTEROBACTIN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 1; Length 72;
Pred. No. 1.1e+02;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EcoGene; EG14353; ybdz.
InterPro: IPR005153; MbtH.
Pfam, PF03621; MbtH; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 72 AA: 8271 MW; 164E0B87E00P1BB8 CRC64;
                                                                 (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: TO M. TUBERCULOSIS MBTH.
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EMBL; M60177; -; NOT_ANNOTATED_CDS.
EMBL; AE000163; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-91175738; PubMed-1826089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 TCQSWSSMIPHWHQRTPENY 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.18;
                                                                                                                                                                           Hypothetical protein ybdz. YBDZ OR B0585.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophytá, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-E-ZO08487; PubMed=10617197; MEDLINDE-ZO083487; PubMed=10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Lin X., Kaul S., Rounsley S.D., Shea T.P., Barnstead M.E., Felddlyum T.V., Bubli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Moffat K.S., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                      Banks B.E.C., Miledi R., Shipolini R.A.;

"The primary sequences and neuromuscular effects of three neurotoxic polypeptides from the venom of Dendroaspis viridis.";

Bur. J. Biochem. 45:457-468(1974).

-1 SUBCELLUAR LOCATION: Secreted.

-1 TISSUE SPECIFICITY: Expressed by the venom gland.

-1 PTM: NEUROTOXIN 4.7.3 DIFFERS FROM 4.9.3 ONLY IN THAT TRP-26 HAS UNDERGONE PARTIAL PHOTOCXIDATION.

-1 MISCELLANBOOS: LD(50) IS 0.9 MG/MG BY INTRAPERITONEAL INJECTION.

-1 SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-cv. C24; TISSUE-Flower buds;
Yu D.Y., Quigley F., Mache R.;
"Isolation and expression of a cDNA encoding protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.5; DB 1; Length 72; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
F299DA0782163B4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THG1_ARATH STANDARD; PRI; 77 AA. 039182; 042011; 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gamma-thionin homolog At2902100 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.2e+
6; Mismatches
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                HSSP, P01386; ITXA.
InterPro, IPR003571; Snake_toxin.
Propin; PF00087; toxin; 1.
Propin; PD000206; Snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
Toxin; Neurotoxin; Multigene family.
                                           MEDLINE=74309059; PubMed=4855008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 KVKAGVGIKCCSTDNC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%;
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31
57
63
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                        SEQUENCE OF 1-30 AND 61-81.
MEDLINE-74055140; PubMed=4763354;
Markussen J., Sundby F.;
"Duck insulin: isolation, crystallization and amino acid sequence.";
Int. J. Pept. Protein Res. 5:37-48(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLILL ROCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-1- CADTION: X'S AT POSITIONS 31-32 AND 59-60 REPRESENT PAIRED BASIC RESIDUES ASSUMED BY HOMOLOGY TO BE PRESENT IN THE PRECURSOR MOLECULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              FULT. J. BIOCHEM. 34:401-408(1973).

-!- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FAITY ACIDS. IT ACCELEAGES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                  suxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
NCBL_TaxID-9839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Long neurotoxin 1 (Neurotoxin 4.7.3/4.9.3).
Dendroaspis viridis (Western green mamba).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae, Elapinae; Dendroaspis.
NCBL_TaxID-8621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                             Markussen J., Sundby F.;
"Isolation and amino-acid sequence of the C-peptide of duck
proinsulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 1; Lengtn a., Pred, No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 IPHWHQRTPENYPNAGLTENYCRNPDSGKQPWCYTTDPCVRWEYCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6EA8A271F099DA91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00049; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
SWARF, SM0078; IGGF, 1.
PROSTIE; PS00262; INSULIN; 1.
Insulin family; Hormone, Glucose metabolism.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Long neurotoxin 1 (Neurotoxin 4.7.3/4.9.3).
                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN A CHAIN. INTERCHAIN.
81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C PEPTIDE.
                                                                                                                   INS.
Anas platyrhynchos (Domestic duck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 PRT;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=73210102; PubMed=4715652;
                                     01, Created)
01, Last sequences 38, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
58
81
80
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 33-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01600; IPDK.
HSSP; P01308; 1HIS
                                     21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                             Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
61
7
19
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NXL1_DENVI
P01394;
 INS_ANAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                       -!- FUNCTION: NEUROTOXIN, BINDS AND INHIBITS NICOTINIC RECEPTORS.
COMPARED TO ALPHA-NEUROTOXINS, KAPPA-NEUROTOXIN BIND MORE STRONGLY
TO NEURONAL RECEPTORS, AND LESS STRONGLY TO NEURONAL RECEPTORS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- IISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 RICLISPS-----STPQTCPNGQDICFRKAQCDNFCHSRGPVIEQGGVATCPQFRSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 RTCQSWSSMIPHWHQRTPENYPNA-----GLITENYCRNPDSGKQPWCYTTDPCVRWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gregoire J., Rochat H., ^{\prime} "Amino acid sequences of neurotoxins I and III of the elapidae snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Naja.
                                                                 Chang L.-S., Lin J., Hong E.; "The exon-intron structure of kappa3-bungarotoxin precursor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 1; Length 87; Pred. No. 1.6e+02;
                                                                                                               Taiwan banded krait.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LONG NEUROTOXIN CR1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S - T (IN REF. 2).
A084F400EFE6BB66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Short neurotoxin 3 (Neurotoxin III) (NWM III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000206; Snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
Toxin; Neurotoxin; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
      Nucleic Acids Res. 18:1050-1050(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Naja mossambica (Mozambique cobra)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003571; Snake_toxin. Pfam; PF00087; toxin: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=78043196; PubMed=923577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X51413; CAA35775.1; -. EMBL; Y11769; CAA72434.1; -. PIR; S08398; B60549. HSSP; P01398; IKBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9660 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
63
79
85
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75 RSLLCC 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 CNLTQC 85
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NXS3_NAJMO
P01432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NXS3_NAJMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
      NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     э;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLIENYCRNPD-----SGKQPWCYTT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 GMGPVTVEARICESOS----HRFKGTCVSASNCA---NVCHNEGFVGGNCRGFRRCFCT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDIJNE-90192091; PubMed-2315018;
Danse J.M., Garnier J.M.;
"CDMA deduced amino-acid sequences of two novel kappa-neurotoxins from Bungarus multicinctus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bungarus multicinctus (Many-banded krait).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Bungarinae; Bungarus.
2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMA-THIONIN HOMOLOG AT2G02100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48.5; DB 1; Length 77; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Long neurotoxin CR1 precursor (Kappa neurotoxin) (Kappa3-
                                                                                                          STRAIN=cv. C24; TISSUB-Flower buds;
Mache R., Quigley F., Thomas F., Yu D.Y.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
EC04E660C3610965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 AA.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00940; GAMMA_THIONIN; 1.
Plant defense; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
  'Sequence and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002118; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00304; Gamma-thionin; 1.
ProDom; PD002594; G_Purothionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X69139; CAA48892.1; -.
EMBL; AC005936; AAC97223.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z18455; CAA79189.1; -.
PIR, S30578; S30578.
HSSP; P20230; 1GPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
77
64
71
73
8524 MW;
                                                                                        SEQUENCE OF 1-75 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00505; Knot1; 1.
                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 28.6
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P15817; P87353;
01-APR-1990 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bungarotoxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
28-FEB-2003
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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79 74

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29; Indels

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InterPro; IPR001421; ATPase8_mit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 DPC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 RNC 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP8_LATCH
003168;
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                           DISULFID
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ATP8_LATCH
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                            FUNCTION: Produces peripheral paralysis by blocking neuromuscular transmission at the postsynaptic site. Binds to the nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.K., KetChum K.A., Lee J.J., Ronning C.M., Koo H.L.,

Moffat K.S., Czronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                     acetylcholine receptor.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed by the venom gland.
--- MISCELLARDGUS: LD(50) is 0.05 mg/kg by subcutaneous injection.
--- SIMILARITY: Belongs to the snake toxin family.
PIR; A01700; NINJ3M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
Submitted (OCT-1992) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                    Toxin; Neurotoxin; Postsynaptic neurotoxin; Multigene family.

DISULEID 3 24 BY SIMILARITY.

DISULEID 17 41 BY SIMILARITY.

DISULEID 43 54 BY SIMILARITY.

DISULEID 55 60 BY SIMILARITY.

SEQUENCE 62 AA; 7218 MW; 06D76622872F7157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.5; DB 1; Length 62;
Pred. No. 1.3e+02;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !- SUBCELLULAR LOCATION: Secreted (Potential).
!- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q41914; Q9ZULG;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATGC02120 OR F504.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 CRNPDSGKQPWCYITDPCVRWEYCNLTQC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CHNOMSAQPP---TTTRCSRWE----TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                    Eur. J. Biochem. 80:283-293(1977).
                                                                                                                                                                                                                                                               Pfam; PF00087; toxin; 1.
ProDom; PD000206; snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
                                                                                                                                                                                                                          430; 1COD.
IPR003571; Snake_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                       P01430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HG2_ARATH
                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GMGPVTVEARICASQS-----QRFKGKCVSDINCENVCHNEGFPGGDCRGFRRCFCT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GISSTIVTGRICQSWSSMIPHWHQRTPENYPNAGLTENYCRNPD-----SGKQPWCYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zardoya R., Meyer A.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZIMATIC COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Coelacanthiformes, Coelacanthidae, Latimería.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                              GAMMA-THIONIN HOMOLOG AT2G02120.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
FY -> D (IN REF. 1).
FY G (IN REF. 1).
FY G (IN REF. 1).
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ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATP8 OR ATP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47.5; DB 1; Length 77;
Pred. No. 1.6e+02;
; Mismatches 28; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Latimeria chalumnae (Latimeria) (Coelacanth) Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 AA.
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                                                                                                                                                                                                                                                                                                                                   PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                  Pfam; PF00304; Gamma-thionin; 1. revobom; P9002594; G_Purothionin; 1. SWART; SW00505; Knotl; 1. PROSITE; PS00940; GAMMA_THIONIN; 1.
                                                                                                                                                                                        Interpro; IPR002118; Gamma-thionin.
Interpro; IPR003614; Knot1.
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                                                                                                             EMBL; AC005936; AAC97222.1; -. PIR; B84433; B84433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8578 MW;
                                                                                EMBL; Z17665; CAA79029.1;
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                                                                                                                                                                                                                                                                                                                                                                   Plant defense; Signal;
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77
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hes 18; Conserv
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SEQUENCE FROM N.A.
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3;
                                                                                                                                  6; Gaps
Pfam; PP00895; AIP-synt_8; 1.

Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.

TRANSMEM 4 24 POTENTIAL.

SEQUENCE 55 AA; 6569 MW; 7FE36319E8AF825B CRC64;
                                                                                          Query Match 8.7%; Score 47; DB 1; Length 55; Best Local Similarity 31.7%; Pred. No. 1.3e+02; Matches 13; Conservative 6; Mismatches 16; Indels
                                                                                                                                                              31 SW---SSMIPHWHQRTPENTPNAGLTENYCR-NFDSGKQPW 67
DR
KW
FT
SQ
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Search completed: September 29, 2003, 08:20:19 Job time: 25 secs

g

64 CHITNSQVRWEYCKTPSCS 82

Search completed: September 29, 2003, 08:19:47 Job time : 83 secs

human respi human respi human respi human respi human respi

Q9iue3 Q9ih96 Q8v5h5 Q8bba3 Q8v5i7

human respi

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Q9jhy3 1 Q8v5i6 | Q9iud1 |

Run

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ALIGNMENTS
                        0910E3
0801B96
0805BA3
0805BA3
080517
080517
0801B3
091B93
091B92
                                                                                                                                                            Q16198
Q9C947
      Q9JHY3
Q8V516
Q9IUD1
                                                                                                                                                                   10
                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLRel. 13,
01-MAY-2000 (TrEMBLRel. 13,
01-MAR-2003 (TrEMBLRel. 23,
                                                                                 22222222
                                                                                                                                                                                                                                  PRELIMINARY;
 PLG protein (Fragment).
                                                                                                                                                                                                                                                                              Homo sapiens (Human).
NCBI_TaxID=9606;
52.5
52.5
52.5
51.5
51.5
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                                                                                                                                                                                                                      RESULT 1
D9UMI2
                                                  (without alignments)
252.503 Million cell updates/sec
                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                         Description
                                           September 29, 2003, 08:11:29; Search time 93 Seconds
                                                                           539
1 KSPVVQDCYHGDGRSYRGIS......DPCVRWEYCNLTQCSETESG
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                 830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                               OM protein - protein search, using sw model
                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                             sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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sp_vertebrate:*
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sp_rodent:*
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Match Length
                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 91
                                                                                              BLOSUM62
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                                                                           Perfect score:
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Oppry3 dendroaspis O9915 human respi O91691 human respi O9168 human respi O9168 human respi O9168 human respi O9168 human respi O9167 human respi O9167 human respi O9167 human respi O9165 human respi O9168 human respi O9169 and respi O9169 human respi O9169 and respi O9169 and respi O8413 sallong sapien O947 arabidopsis O947 arabidopsis O9473 sallong sallar

[1]
MEDLINE-8502311; PubMed=6148961;
MEDLINE-8502311; PubMed-6148961;
Malinowski D.P., Sadler J.E., Davie E.W.;
Malinowski D.P., Sadler J.E., Davie E.W.;
"Characterization of a complementary deoxyribonucleic acid coding for Gaps Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrinii; Hominidae; Homo. · 0 Length 53; Indels 2EB36E715CD40A47 CRC64; Last sequence update) Last annotation update) Score 236; DB 4; Pred. No. 3.4e-19; 43.8%; Scc... 81.6%; Pred. No. 3... 4; Mismatches AA. human and bovine plasminogen."; Biochemistry 23:4243-4250(1984). -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. 23 PROSITE; PSO0021; KRINGLE_1; FALSE_NEG. PROSITE; PS50070; KRINGLE_2; 1. Created) PRT; InterPro; IPR000001; Kringle. Pfam; PF00051; Kringle; 1. PRINTS; PR00018; KRINGLE. ProDom; PD000395; Kringle; 1. 53 AA; 5893 MW; EMBL; K02921; AAA60123.1; -. HSSP; P00747; 2PK4. 40; Conservative Glycoprotein; Kringle.
NON_TER 1 1
SEQUENCE 53 AA; 589 SMART; SM00130; KR; 1 Local Similarity Query Match Matches DDT HERE THE PRICE OF THE PRICE

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2 SPVVQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPNA

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Q8bba4 human respi Q9dfel oncorhynchu Q39403 brassica ca Q8v5i2 human respi Q8bba8 human respi

Q8BBA4 Q9DFE1 Q39403 Q8V512 Q8BBA8

Q8sq84 gorilla gor Q8bba5 human respi

Q30599 macaca mula 019292 macaca mula

Q8MVA6 Q8V5I3 Q30599 O19292 Q8SQ84

443.8 338.5 222.4 222.6 220.4 220.7 200.0 111.0 111.0 111.0 110.0

111111100876543

99ukj7 homo sapien Q9bgn9 bos taurus Q9ud88 homo sapien Q8mva6 ixodes scap Q8v5i3 human respi

Q9umi2 homo sapien Q8ng20 homo sapien

Q9UMI2 Q8NG20 Q9UKJ7 Q9BGN9 Q9UD88 respi

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Gaps

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Q8NG20

RESULT 2

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Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Uterus;
Murakami S., Fujiwara C., Miyamoto Y., Takeuchi S., Takahashi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
APO(A) KRINGLE 4-37, APO(A) KRINGLE type 5 (Fragment).
Buno sapias (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression and action of hepatocyte growth factor in bovine endometrial stromal and epithelial cells in vitro."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ABO56447; EMBBJ3031.1; -. HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 120.5; DB 6; Length 75; Pred. No. 4e-06;
                                                                                                                                         DB 4; Length 60;
                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                              60 60
60 AA; 6799 MW; 5719AA26B3E0FF1D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hepatocyte growth factor (Fragment).
                                                                                                                                                                                                          51 GLTENYCRNPDSGKQPWCYTTDPCVRWEYCNLTQCSETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 NYCRNPDSGKQ--PWCYTTDPCVRWEYCNLTQCSETE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9e-14;
                                                                                                                             34.9%; Scor. 77.5%; Pred. No. >c. 77.5%; Pred. No. >c. 77.5%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AA.
                                                                                                                                                                                                                                                                                                                             75 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel, 17, Created)
SMART; SM00130; KR; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS50070; KRINGLE_2; 1.
Glycoprotein; Kringle; Lipoprotein.
NON_TER
                                                                                                                                                                                                                                                                                                                               * PRT;
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ProDom; PD000395; Kringle; 2.
SMART; SW00130; KR; 2.
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56.8%;
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                                                                                                                                                                         31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Kringle.
                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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SEQUENCE
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NON_TER
SEQUENCE
                                                                                                                                           Query Match
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                                                                                                                                                                         Matches
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Q9BGN9
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        DR WE BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 DCYHGDGRSYRGISSITVTGRICQSWSSMIPHWHQRIPENYPNA---GL-TENYCRNPDS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
   ch 38.5%; Score 207.5; DB 4; Length 90; 1 Similarity 47.6%; Pred. No. 9.2e-16; 40; Conservative 14; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                      "Production of kringle fragment.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
EMBL, AF202803; AMM5248.1;
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InterPro; IPR000001; Kringle.
Pram; PR00051; kringle; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Kringle.
SEQUENCE 90 AA; 9804 MW; A33887F9FDF4C7B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEWBLrel. 13, Created)
01-WAY-2000 (TrEWBLrel. 13, Last sequence update)
01-WAR-2003 (TrEWBLrel. 23, Last annotation update)
                                                                                                                                    01-0CT-2002 (TIEMBLRel. 22, Created)
01-0CT-2002 (TIEMBLRel. 22, Last sequence update)
01-MAR-2003 (TIEMBLRel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AA.
                                                                                                        90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GKOPWCYTTDPCVRWEYCNLTQCS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||||||:| ::||: DARPWCYITNPRKLYDYCDVPQCA 89
                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=21181705; PubMed=11285247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00021; KRINGLE_1; 1. PROSITE; PS50070; KRINGLE_2; 1.
                                                                                                                                                                                         Plasminogen/activator kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00001; Kringle.
Pfam; PF00051; Kringle; 1.
ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Venter M., Madhi S.A., Tiemessen C.T., Schoub B.D.; "Genetic diversity and molecular epidemiology of respiratory syncytial virus over four consecutive seasons in South Africa: identification of
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97152405; PubMed-8995183; Knapp L.A., Cadavid L.F., Eberle M.E., Knechtle S.J., Bontrop R.E., Watkins D.I., "Identification of new mamu-DRB alleles using DGGE and direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 YHGDGRSYRGISSTTVTGR-TCQSWSSMIPHWHQRTPENYPNAGLTENYCRN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 FDSDVGEYRAVSE---LGRPTAESWNSQKDYLEQK-----RGQVDNYCRH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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Ω
                                                                                                                                                                                                                                                                                                                                       1 KSPVVQDCYHGDGRSYRGISSTTVTGRICQSWSSMIPHWHQRTPENYPNAGLT
                                                                                                                                                                                                                                                                                                                                                                           21 KKPTPKTTERGTSTSQSTVLDTTTSKHTIQQQS----LHSTTPENTPNSTQT
                                                                                                                                                                                                                                                           DB 12; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 82;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                    CEF8B4DD27344769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TremBirel. 01, Created)
01-NOV-1996 (TremBirel. 01, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
Major histocompatibility complex class II. (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA; 9945 MW; 1FE11A6520A60108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II DR beta (Fragment).
HLA-DRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 59.5; DB
30.8%; Pred. No. 29;
tive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AA.
                                                                                                                                                                                                                                                         Query Match 11.2%; Score 60.5; Dest Local Similarity 32.1%; Pred. No. 24; Matches 17; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PD000328; MHC_II_beta; 1. Glycoprotein; MHC_II; Transmembrane. NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                new subgroup A and B genotypes.",
J. Gen. Virol. 82:2117-2124(2001).
EMBL; AF348815; AAL60316.1;
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; I.
NON_IER
                          MEDLINE=21405813; PubMed=11514720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U57941; AAC50974.1; -.
InterPro, IPR000353; MHC_II_beta.
Pfam; PF00969; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing.";
Immunogenetics 45:171-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                    87 AA; 9431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 30.8 es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC-DRB.
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019292
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
030599
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Rhode Island; TISSUB-Salivary gland;
Valenzuela J.G., Francischetti I.M., Pham V.M., Garfield M.,
Mather T.M., Ribeiro J.M.G.;
"Exploring the Sialome of the Tick Vector of Lyme Disease, Ixodes
                                                                                          Pfaffinger D., Mc Lean J., Scanu A.M.; "Amplification of human APO(a) Kringle 4-37 from blood lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative 5.3 kDa secreted protein.

Fuddes scapularis (Black-legged tick) (Deer tick).

Eukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

Parasitiforms; Ixodida; Ixodidae; Ixodes.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%; Score 62; DB 5; Length 69; 35.0%; Pred. No. 13; Live 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scapularis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF483734; AAM93656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSGKQPW-----CYTTDPCVRWEYCNLTQCSETESG 91
                                                                                                                                                                                                                                                                         25 25
25 AA; 2928 MW; BEEDD4C62FA480A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 AA; 7817 MW; EBB93FDBFA754E24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMELrel. 22, Created)
01-OCT-2002 (TrEMELrel. 22, Last sequence update)
01-OCT-2002 (TrEMELrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   Score 109; DB 4;
Pred. No. 2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                      Biochim, Biophys, Acta 1225:107-109(1993).
HSSP, P00747; TKRN.
InterPro; IPR000001; Kringle.
Pfam; PP00051; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attachment glycoprotein G (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                             68 CYTIDPCVRWEYCNLTQCSETE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus.
                                                        SEQUENCE FROM N.A.
MEDLINE=94060120; PubMed=7848387;
                                                                                                                                                                                                                                                                                                                                   20.2%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                       ycoprotein; Kringle
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                      NCBI_TaxID=9606
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter M., Collinson M., Schoub B.D.;
"Molecular epidemiological analysis of community circulating
"Molecular epidemial virus in rural South Africa: Comparison of
viruses and genotypes responsible for different disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter M., Collinson M., Schoub B.D.;
"Molecular epidemiological analysis of community circulating respiratory syncytial virus in rural South Africa: Comparison of viruses and genotypes responsible for different disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 KKPTPKITERGISISQSTVLDTITSKHTIQQQS-----LHSTTPENTPN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSPVYQDCYHGDGRSYRGISSTTVTGRTCQSWSSMIPHWHQRTPENYPN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
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Pred. No. 40;
3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AA; 9431 MW; F72B9DC59C975EE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 AA; 9491 MW; 3BFFB3AD57345C68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEWELrel. 23, Created)
01-WAR-2003 (TrEWELrel. 23, Last sequence update)
01-WAR-2003 (TrEWELrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58.5; DB Pred. No. 40; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AA
                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AgK6-99;
MEDLINE=22213634; PubMed=12226836;
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MEDLINE=22213634; PubMed=12226836;
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J. Med. Virol. 68:452-461(2002).
EMBL; AF548807; AAN62464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          manifestations,";
J. Med. Virol. 68:452-461(2002).
EMBL; AF548806; AAN62463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.9%;
Best Local Similarity 32.7%;
Matches 16; Conservative
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32.7%;
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Best Local Similarity 32.7
Matches 16; Conservative
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                                                                                                                                                                                                                                              PRELIMINARY;
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      72 DPCVRW 77
                                                                           63 GTCVEW 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                             MEDLINE-94179810; PubMed-8133043;
MEDLINE-94179810; PubMed-8133043;
Slarendragt B.L., Otting N., van Besouw N., Jonker M., Bontrop R.E.;
"Expansion and contraction of rhesus macaque DRB regions by
dunification and deletion.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arnaiz-Villena A., Martinez-Laso J., Alvarez M., Castro M.J.,
Varela P., Gomez-Casado E., Suarez B., Recio M.J., Vargas-Alarcon G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59.5; DB 7; Length 82;
Pred. No. 29;
8; Mismatches 17; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBL_TaxID=9593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 YHGDGRSYRGISSTTVTGR-TCQSWSSMIPHWHQRTPENYPNAGLTENYCRN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 FDSDVGEYRAVSE---LGRPTAESWNSQKDYLEQKRAE------VDNYCRH 74
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 10.9%; Score 59; DB 6; Length 78; 1 Similarity 22.7%; Pred. No. 31; 15; Conservative 10; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood; de Groot N.N.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF031268; ABB97440.1; -. HSSP; P13758; 1DLH.
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82 AA; 9960 MW; 71FA3A6520A60119 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC_II_Transmembrane.
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MEDLINE=97364681; PubMed=9218527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000353; MHC_II_beta.
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EMBL; L41256; AAL77572.1; -.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Primate Mhc-E and -G alleles.";
                                                                                                                                                                                                                                                                                                     duplication and deletion.";
J. Immunol. 152:2298-2307(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00129; MHC_I; 1. ProDom; PD000050; MHC_I; 1.
                                                                                                                                      SEQUENCE OF 3-30 FROM N.A.
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                                         Cercopithecinae; Macaca
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MHC-G.
                                                                        NCBI_TaxID=9544;
                                                                                                                                                                         TISSUE-Blood;
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01-JUN-2002
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NON_TER
SEQUENCE
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                                                                                                              72 DPC 74
                                                                                                                                                        75 RHC
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Matches
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Bayne C.J., Gerwick L., Fujiki K., Nakao M., Yano T.;
Immune-relevant (including acute phase) genes identified in the livers of rainbow trout, Oncorhynchus mykiss, by means of suppression subtractive hybridization.';
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR281349; AAG30024.1.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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"Nucleotide sequences of protease inhibitor II in chinese cabbage.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Creament).
01-Crype lectin 2-1 (Fragment).
01-Crype lectin 2-1 (Fragment).
01-MARIS (Rainbow trout) (Salmo gairdneri).
01-MARINOTENTALI).
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Pred. No. 45;
5; Mismatches 25; Indels 13;
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&
                         64
Score 58; DB 13; Length 64;
Pred. No. 33;
9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
64 AA; 7555 MW; 1D3D9811059B5FD9 CRC64;
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01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
Protease inhibitor II.
Brassica campestris (Field mustard).
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InterPro; IPR003614; Knot1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00304; Gamma-thionin; 1.
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31.7%;
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Best Local Similarity 26.9%;
Matches 14; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8453 MW;
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HSSP; P20230; 1GPT.
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Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3711;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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18 GISSTIVTGRICQSWSSMIPHWHQRIPENYPNAGLTENYCRNPD-----SGKQPWCYIT 71
                                                   22 GMGPVTVEARTCESKS----HRFKGTCVSSTNCG---NVCHNEGFGGGKCRGFRVRCYCT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SA98D661;
MEDLINE-21405813; PubMed-11514720;
Venter M., Madhi S.A., Tiemessen C.T., Schoub B.D.;
"Genetic diversity and molecular epidemiology of respiratory syncytial virus over four consecutive seasons in South Africa: identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 83 AA; 9057 MW; 9ADE60D26C24E4AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Attachment glycoprotein G (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57.5; 1
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        new subgroup A and B genotypes.";
J. Gen. Virol. 82:2117-2124(2001).
EMBL; AFS48816; AALG0317.1;
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; I.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human respiratory syncytial virus.
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32.1%;
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September 29, 2003, 08:22:53 ; Search time 82 Seconds (without alignments) 172.276 Million cell updates/sec
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| SIDSI/Ggddata/geneseqfygeneseqfy-embl/AA1980.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1980.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1991.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA192.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1992.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1995.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1995.bAT:*
| SIDSI/Ggddata/geneseqfygeneseqp-embl/AA1995.bAT:*
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| SIDSI/gcgdata/geneseg/geneseqp-embl/AA1988.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: /SIDS1/παπΑπάττ.'-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                          Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human apolipoprote	Human plasminogen	Plasminogen kringl	Amino acid sequenc	Human kringle 4.	Murine kringle 4.	Human ORFX protein	Murine krindle 3.	Porcine kringle 3.
SUMMARIES	qi	AAY72946	AAY77720	AAP93231	AAB08414	AAW07560	AAW07559	ABP02801	AAW07554	AAW07557
	B :	22	21	10	21	17	17	23	17	17
	re Match Length DB I	89	84	82	83	78	78	98	78	78
\$ Query	Match	100.0	82.2	81.6	80.5	79.7	9.07	8.99	59.8	57.2
	Score	523	430	427	421	417	369	349.5	313	299
Result	No.		7	m	4	Ŋ	9	7	ω	σ

Human plasminogen	Human kringle 3.	Rhesus kringle 3.	Bovine kringle 3.	Bovine kringle 2.	Amino acid sequenc	Porcine kringle 2.		ID 113 of	ultifunc	Human plasminogen	Plasminogen kringl	Human plasminogen	Rhesus kringle 1.	human kringle 1.	Human kringle 2.	Human plasminogen	K1 domain of plasm	Plasminogen kringl	Rhesus kringle 2.	plasminog	Murine kringle 2.	Bovine kringle 1.		Sequence encoding	Amino acid sequenc	Porcine kringle 1.	murine kringle 1.	Human plasminogen	Amino acid sequenc	Amino acid sequenc	Human apolipoprote	Human liver peptid	#42	#432	
AAB01908		AAW07556	AAW07558	AAW07553	AAB08412	AAW07552	AAY02134	AAY02133	AAY02110	AAY77719	AAP93230	AAB01906	AAW07546	AAW07545	AAW07550	AAB01907	AAP81360	AAR96221	AAW07551	AAY77721	AAW07549	AAW07548	AAP90598	AAP94401	AAB08410	AAW07547	AAW07544	AAW19256	AAB08413	AAB08411	AAY72947	ABG51665	ABB31599	88	ABB22143
23	17	17	17	17	21	17	20	20	20	21	10	21	17	17	17	21	σ	17	17	21	17	17	10	10	21	17	17	18	21	21	22	22	22	22	22
83	78	78	78	78	83	78	8 8 8	8	88	82	84	84	79	79	78	82	79	79	78	78	78	79	81	78	84	79	79	79	82	82	86	25	25	52	52
	54.5								51.9								50.2		50.1					48.7		47.3			45.9	ď.	-	ď			
286	285	283	281	277	276	274	271.5	271.5	271.5	269.5	269.5	269.5	268.5	267.5	264	264	262.5	262.5	262	261	260	256.5	256	254.5	253.5	247.5	245.5	244	240	236	224	223	223	223	. 223
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Human; anglogenesis inhibitor; LK7; apolipoprotein(a) kringle domain; anglogenesis-mediated disease; cancer; rheumatoid arthritis; therapy; cytostatic, antirheumatic; antiarthritic; antipsoxiatic; psoxiasis; ocular anglogenic disease; endothelial cell proliferation; tumour; cell migration.
                                                                                          Human apolipoprotein(a) kringle domain IV37, LK7 protein.
                                                                                                                                                                                                                                                                                                                                 Yum J, Chung S;
                                                                                                                                                                                                                                                                                                          (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                     AAY72946 standard; Protein; 89 AA.
                                                                                                                                                                                                                                                                                                                                Chang J, Kim JS, Park EJ,
                                                                                                                                                                                                                                                           99WO-KR00554
                                                                                                                                                                                                                                                                                 99WO-KR00554
                                                                    (first entry)
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N-PSDB; AAD03257.
                                                                                                                                                                                                            WO200119868-A1.
                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                         15-SEP-1999;
                                                                                                                                                                                                                                                                                 15-SEP-1999;
                                                                    13-JUN-2001
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                                            AAY72946;
RESULT 1
        AAY72946
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kringle 4; plasminogen; anti-angiogenic; angiogenesis; angiostatin; cytostatic, antiarhirtic; antizheumatic; antidabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; antiarteriosclerotic; human; dermatological; cancer; tumour; birth control; vascularization.
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                                                                                                                                                                                                                                                                                                                                                                                      1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT 60
                                                                                                      The present sequence is human LK7 protein which contains the amino acid sequence of human apolipoprotein(a) kringle domain LY37 (LK1V37). The human apolipoprotein(a) kringle domains LY36 (LK6 protein), 1V37 (LK7 protein) and V38 (LK8 protein) together form the angiogenesis inhibitors LK68 protein. LK68, LK6, LK7 and LK8 are inhibitors are of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo choricallantoic membrane (CAM). LK68 protein, its single kringles or their functional equivalents, are useful for treating angiogenesis-mediated diseases, such as cancer, rheumatoid arthritis, psociasis or coular angiogenic disease in animals or humans. LK68 is useful as an anticancer agent and
            Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
                                                                                                                                                                                                                                                                                                                                                                      1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel lysine binding fragments angiostatin used as antiangiogenic agents in the treatment of cancer, diabetic retinopathy, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "specifically claimed fragment (AAY77723)"
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0
                                                                                                                                                                                                                                                                                                                   Length 89;
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                                                                                                                                                                                                                                                                                                              100.0%; Score 523; DB 22;
100.0%; Pred. No. 5.2e-46;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GPWCFITDPSIRWEYCNLTRCSDTEGIVV 89
                                                                                                                                                                                                                                                              also for inhibiting primary tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human plasminogen kringle 4 sequence
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                                                                                Claim 2; Page 45-46; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY77720 standard; protein; 84 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 89; Conservative
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                                                                                                                                                                                                                                                                                        89 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1998;
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Region
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The invention provides fragments of kringle 1, 2 or 4 of human plasminogen that contain a lysine binding site and have anti-angiogenic activity. The peptides of the invention function as antiangiogenic agents, for the treatment process and diseases involving angiogenesis. Such diseases include cancers such as solid timours, blood born tumours such as leukemias, tumours metastasis, benign tumours such as themangiomas, acoustic acuromas, neurofilbromas, trachomas and pyogenic granulomas, rheumatoid arthritis, ocular angiogenic diseases such as dabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber syndrome, myocardial angiogenesis, plaque neovascularization, telangiectasia, hemophiliac joints, angiofibroma, and wound granulation. The fragments are also useful in treatment of disease of axcessive or abnormal stimulation of endothelial cells. These disease include intestinal adhesions, atherosclerosis, soleroderma, and hypertrophic scars. The fragments can be used as birth control agents by preventing vascularization required for embryo transplantation. The present sequence of human plasminogen
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arthritis, psoriasis, atherosclerotic plaque formation, and other angiogenesis diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified plasminogen activator - having greater fibrin selectivity and circulating halflife.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen; activator; t-PA; flbrin; kringle domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen kringle 4 domain (residues 354-435).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 430; DB 21;
Pred. No. 1.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GPWCFTTDPSIRWEYCNLTRCSDT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GPWCFTTDPSVRWEYCNLKKCSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP93231 standard; peptide; 82 AA.
                                                                                                                                      Disclosure; Fig 3; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLB ) COLLABORATIVE RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0184823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89WO-US01255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abercrombie DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-339965/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN92238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (angiostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
03-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO8910401-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-NOV-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP93231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mao JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scu-PA;
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Castleman's disease,
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                                                                                                                                                                                                                                                                                                                                                                            AAW07560;
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                                                                       Seguence
                                                                                                     Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cao I,
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                AAW07560
                                                                                                                                                                                                                                                                                                              RESULT
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                                                The sequence is encoded by a synthetic oligonucleotide and is the kringle 4 domain of plasminogen. It is used to construct a modified plasminogen activator (mPA) of greater fibrin selectivity than normal PA. The mPA is used in the treatment of pulmonary embolism, thrombosis, myocardial
                                                                                                                                                                                                                                                            1 VRQCYHGNGQSYRGIFSITVIGRICQSWSSWIPHRHQRIPENYPNDGLIMNYCRNPDADI 60
                                                                                                                                                                                                                                                                               The specification describes a human polypeptide which is a potent anglogenesis inhibitor, and is designated KED. KED polypeptide, Kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit anglogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KD is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anglogenesis inhibitor; KED; kringle protein; anglogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangloma.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                ò
                                                                                                                                                                                                Length 82;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of kringle 4 of human plasminogen.
                                                                                                                                                                                                Score 427; DB 10; Pred. No. 3.1e-36; 5; Mismatches 7;
                                                                                                                                 (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dou D, Chopp M, Wang L, Mikkelsen T;
                   Disclosure; fig 3b; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 6; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08414 standard; Protein; 83 AA
                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FORD-) FORD HEALTH SYSTEM HENRY.
                                                                                                                                                                                                                                                                                                                           GPWCFTTDPSIRWEYCNLTRC
                                                                                                                                                                                                                                                                                                                                                           GPWCFTTDPSVRWEYCNLKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0121341.
99US-0121633.
99US-0166176.
                                                                                                                                                                                                81.6%;
85.2%;
                                                                                                                                                                                                                                                                                                                                            24-FEB-2000; 2000WO-US04798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                              Local Similarity 85.2
Hes 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-572016/53.
                                                                                                                  strokes
                                                                                                                                                                 82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200049871-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2000
                                                                                                                    infarct and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB08414;
                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                  Sequence
                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                          AAB08414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQQCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNNGLTMNYCRNPDADK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or human, Rhesus, porcine or bovine plasminogen and is a kringle 1.2, kringle 2.3, kringle 1.2, kringle 2.3, kringle 1.2, kringle 1.2, kringle 2.3, kringle 2.3, kringle 1.2, kringle 1.2, kringle 2.3, kringle 2.3, kringle 1.2, kringle 1.2, kringle 2.3, kringle 2.3, kringle 1.2, kringle 2.3, kringle 2.3, kringle 1.2, kringle 1.2, kringle 2.3, kri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangioma. The present sequence represents kringle 4 of human plasminogen, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies for use in diagnosis, detection and therapy.
The present sequence, human kringle 4, is a specific angiostatin fragment which can be used in the invention.
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                                                                                                                                                                                                                                                                                                                  Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                             Score 421; DB 21;
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPWCFTTDPSIRWEYCNLTRCS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 116; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPICFITDPSVRWEYCNLKKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW07560 standard; protein; 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                        80.5%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US05856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0612788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                          83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kringle 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-1996;
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                                                                     4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                       1 CYHGDGQXXRGISSTITTGKKCQSWSSMIPHRHQKIPENIPNAGLIMNYCRNPDADKGPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 2, kringle 1-3, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-2, kringle 1-4 or kringle 1-4 mino acid number 98 of murine, human, Rhesus, porcine of bovine plasminogen. The active component can be used for treating anglogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                             angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degeneration and diabetic retinopathy. It can also be used to deverantibodies for use in diagnosis, detection and therapy. The present sequence, murine kringle 4, is a specific angiostatin fragment which can be used in the invention, and represents amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                   0;
Score 417; DB 17; Length 78;
Pred. No. 3e-35;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim KL;
                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao Y, Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids 377-454 of murine plasminogen.
                                                                                                                                                                                                                                                        AAW07559 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 115; 203pp; English.
                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIL-) CHILDRENS MEDICAL CENT
79.7%;
                                                                                                                                      64 CFTIDPSIRWEYCNLIRC
                                                                                                                                                         CFTTDPSVRWEYCNLKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0612788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US05856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0429743
96US-0605598
                                                                                                                                                                                                                                                                                                                            22-JUN-1997 (first entry)
                                   67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-518662/51.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AA;
                                                                                                                                                                                                                                                                                                                                                            Murine kringle 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-1996;
26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1996.
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                                   Matches
                                                                                                                                                                                                                        RESULT 6
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Gaps

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11; Indels

70.6%; Score 369; DB 17; 73.1%; Pred. No. 2.4e-30; Live 10; Mismatches 11;

Conservative

Query Match
Best Local Similarity
Matches 57; Conserv

Length 78;

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABM15762 to ABM27252 encode the human OREX proteins given in ABP00010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide syndrome associated with ORFX-associated disorder. ORFX polynucleotide treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders, infectious transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester stroage disease, various immune disorders and disorders, infectious also disease and autoimmune disorders with a multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Ost transitis autoimmune manulamenter experience in the protein and autoimmune inflammatory eye disease. Ost transitis and disconders in the protein and autoimmune inflammatory eye disease. Ost transitis and autoimmune inflammatory eye disease. Ost transitis and disconders in the protein and autoimmune inflammatory eye disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorthage; degenerative disorder; osteoarthrits; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypertyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                               useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX protein sequence SEQ ID NO:5584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 5584; 1037pp; English.
                                                                                                                                                                                                                                                                                                    ABP02801 standard; Protein; 86 AA.
                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000; 2000US-206132P. 29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001WO-US10836.
                                                                                                             64 CFTTDPSIRWEYCNLTRC
                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABN18553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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acids 275-352 of murine plasminogen or amino acids 178-255 of murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9635774-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1996;
                           angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW07557;
                                                                              Seguence
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                                                                                                                              Query Match
                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y,
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW07557
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                                                                                                                                                                                                                                                  Ä
                                                                                                                                                                                                                                                                                                59
                                                N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                            1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDAD-
                                                                                                                                                                                                                                                  Gaps
reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                Length 86;
                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim KL;
                                                                                                                                                                                             66.8%; Score 349.5; DB 2373.4%; Pred. No. 2.7e-28; ive 8; Mismatches 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao Y, Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW07554 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 111; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           60 TGPWCFTTDPSIRWEYCNL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                      67 RGPWCFTTDPSVRWEYCNL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0612788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0429743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US05856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1997 (first entry)
                                                                                                                                                                                                                      Local Similarity 73.4 nes 58; Conservative
                         systemic cytokine damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine kringle 3.
                                                                                                                                                86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW07554;
                                                                                                                                                  Sequence
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragment, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 1, kringle 0, mr. kringle 0, mr. kringle 1, kringle 2, kringle 3, kringle 3, kringle 3, kringle 3, kringle 3, kringle 2, kri
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                    1 CLKGRGENYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNPDGETAPW 60
                                                                                                                                                                                                                                                                                                                       4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
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                                                                                                                                                                                                             ö
                                                                                                         Length 78;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim KL;
                                                                                              Score 313; DB 17;
Pred. No. 1.3e-24;
9; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 113-114; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids 178-255 of porcine angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW07557 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0612788.
95US-0429743.
96US-0605598.
                                                                                                         59.88;
                                                                                                                                                           61,5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US05856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                           L Similarity 61.5
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine kringle 3.
78 AA;
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ó 62 62

Gaps

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Indels

Score 286; DB 21; Pred. No. 7.9e-22; 9; Mismatches 26;

Length 83;

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3 QCLKGTGENYRGNVAVTVSGHTCQHWSAQTPHTHNRTPENFPCKNLDENYCRNPDGKRAP
                                                                                                                           3 QCYHGNGQSYRGTFSTIVTGRICQSWSSMTPHRHQRIPENYPNDGLIMNYCRNPDADIGP
full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                 63 WCHIINSQVRWEYCKIPSC 81
                                                                                                                                                                                  63 WCFTTDPSIRWEYCNLTRC 81
                                                                                                  44; Conservative
                                                                                   Similarity
                                          AA;
                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1996;
26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       21-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present
 the
                                                                                                                                                                                                                                                                                                              AAW07555;
              figure 1.
                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                       Query Match
                                                                                     Best Local
                                                                                                  Matches
                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                      AAW0755
88868
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                                                                                                                                                                                  δă
                                                                                                                                                                                                                                                                                   The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastases in the ratio 1:100-1:300, followed by incubating and isolating to the fragment. The kringle 5 peptides are inhibitors of angiogenesis and enothelial cell proliferation and migration. The peptides are useful for treating angiogenic diseases, primary and metastatic solid tumours of and carcinomas of various organs such as breast, genifical temours and carcinomas of various organs such as leukaemias and carcinomas of various used for the brain and eyes and solid tumours arising from haematopoletic malignancies such as leukaemias and lamphomas. They are also used for the prophylaxis of various autoimmus (1900, promises of e.g., rheumatoid arthitis), coular diseases (e.g., rheumatoid arthitis), coular diseases, skin diseases (e.g., rheumatoid arthitis), coular diseases, skin diseases (e.g., rheumatoid arthitis), ocular diseases, skin diseases (e.g., rheumatoidenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agant which inhibits ovullation and satablishment of the placenta.

Comported the prophilation and astablishment of the placenta.

Composition of the invention.

Composition of the invention.
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                                                                                                                                                                                                                                                                                                                                     Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; oytostatic; antiproriatic; antilnflammatory; antiulcer; antirheumatic; antiarthritic; antiangiogenic; cancer; tunnour; autoimmune disease.
                                                                      63
                                                                                     1 CLKGRGENTRGTVSVTASGHTCQRWSAQSPHKHNRTPENFPCKNLEENYCRNPDGEJAPW 60
                                                                    4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, ocular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by
                                          ;
             Length 78;
                                          Indels
             57.2%; Score 299; DB 17;
56.4%; Pred. No. 3.5e-23;
ive 12; Mismatches 22;
                                                                                                                                                                                                                                                                                                           Human plasminogen kringle 3 (Thr253-Ser335).
                                                                                                                                                                                                                          AAB01908 standard; Protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 17; Page -; 48pp; English.
                                                                                                                                         |:||| :||:|| CYTTDSEVRWDYCKIPSC 78
                                                                                                                           CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0851350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0643219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0832087
                                                                                                                                                                                                                                                                               18-SEP-2000 (first entry)
                                          44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           incubation and isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT LAB.
                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                      US6057122-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2000
                                                                                                                           64
                                                                                                                                                    61
                                                                                                                                                                                                                                                      AAB01908;
                Query Match
                                                                                                                                                                                                RESULT 10
                                          Matches
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Inhibiting endothalial call proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 2-3, kringle 1-3, kringle 1-48KLS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiostation and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy
                                                                                                                                                                                                                                                                                                                     angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence, human kringle 3, is a specific angiostatin ich can be used in the invention, and represents amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new methods and compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao Y, Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids 178-255 of human angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 112; 203pp; English.
AAW07555 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIL-) CHILDRENS MEDICAL CENT.
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96US-0605598.
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                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA;
                                                                                                                                                                                                                                             Human kringle 3.
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9

Best Local Similarity

Matches

g à g

Query Match

Rhesus kringle 3.

AAW07556;

RESULT 12

WO9635774-A2.

Rhesus

14-NOV-1996.

26-APR-1996; 08-MAR-1996; 26-APR-1995; 22-FEB-1996;

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1 CLKGTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENYCRNPDGEKAPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1.2, kringle 2.3, kringle 1.2, kringle 1.2, kringle 1.2, kringle 1.4 or kringle 1.4
        4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW
                                             4 CYHGNGQSYRGIFSIIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDADIGPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies for use in diagnosis, detection and therapy.
The present sequence, bovine kringle 3, is a specific angiostatin
fragment which can be used in the invention, and represents amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sim KL;
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; Pred. No. 2.4e-21;
11; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids 178-255 of bovine angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 114; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW07558 standard; protein; 78 AA.
                                                                                                                                                              81
                                                                                                                                                                                                            |:||: :||||: |
61 CYTTNSQVRWEYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.7%;
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95US-0429743.
96US-0605598.
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                                                                                                                                                                  64 CFTIDPSIRWEYCNLTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-518662/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine kringle 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW07558;
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                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, Rhesus kringle 3, is a specific angiostatin fragment which can be used in the invention, and represents amino
                                                                                                                                                              4 CYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRIPENYPNDGLTMNYCRNPDADTGPW
                                                                                                                                                                                                            Gaps
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    Length 78;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sim KL;
54.5%; Score 285; DB 17;
55.1%; Pred. No. 9.3e-22;
iive 10; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Pages 112-113; 203pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW07556 standard; protein; 78 AA.
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                                                                                                                                                                                                                                                                                                                         81
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96US-0605598.
                                                                                                                                                                                                                                                                                                                                                                                                61 CHTINSQVRWEYCKIPSC
                                                                                                                                                                                                                                                                                                                         64 CFTTDPSIRWEYCNLTRC
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                                                                                   43; Conservative
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WPI; 1996-518662/51.

AAWO7556

XX AAW

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Gaps

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78 AA;

Sequence

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81

CFTTDPSIRWEYCNLTRC

64

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Search completed: September 29, 2003, 08:33:33 Job time: 83 secs
                                                                                                                                                                                                                                                                                                    25-FEB-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                          24-FEB-1999;
                                                                                                                                                                                                                                           31-AUG-2000.
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                                                AAB08412;
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 RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, accombination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 23, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4 bKLS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid unmber 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CMHCSGENYEGKIAKTWSGRDCQAWDSQSPHAHGYIPSKFPNKNIKMNYCRNPDGEPRPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CYHGNGQSYRGTFSTTVIGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anglogenesis-mediated diseases such as cancer, arthritis, magniar degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy.

The present sequence, bovine kringle 2, is a specific anglostatin fragment which can be used in the invention, and represents amino acids 88-165 of bovine anglostatin.
                                                                                                                                                                    angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                     Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                          Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.0%; Score 277; DB 17;
52.6%; Pred. No. 6.1e-21;
tive 13; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                        Cao Y, Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 110; 203pp; English.
                                                                     AAW07553 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTTNSEVRWEYCTIPSC 78
                                                                                                                                                                                                                                                                                                                                                 (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                              950S-0429743.
                                                                                                                                                                                                                                                                             96WO-US05856.
                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-518662/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AA;
                                                                                                                                            Bovine kringle 2.
                                                                                                                                                                                                                                                                            26-APR-1996;
                                                                                                                                                                                                                                                                                                              26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                             WO9635774-A2
                                                                                                                    21-JUN-1997
                                                                                                                                                                                                                                                                                                  08-MAR-1996;
                                                                                                                                                                                                                                                     14-NOV-1996
                                                                                                                                                                                                       Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                             AAW07553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis inhibitor, and is designated KED. KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (LPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                            tissuė plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distress syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QCYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cattleman's disease, psoriasis, hepatitis, anerrysm, renal disease and haemangioma. The present sequence represents kringle 3 of human plasminogen, which is used in the course of the invention.
                                                                                                                                                                                                                                                             Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification describes a human polypeptide which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Indels
                                                                                                                                                                                              Amino acid sequence of kringle 3 of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 276; DB 21;
Pred. No. 8.3e-21;
8; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dou D, Chopp M, Wang L, Mikkelsen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6; 163pp; English.
   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FORD-) FORD HEALTH SYSTEM HENRY.
AAB08412 standard; Protein; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 WCHTINSQVRWEYCKTPSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 WCFTTDPSIRWEYCNLTRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0121341.
99US-0121633.
99US-0166176.
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55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-2000; 2000WO-US04798
                                                                                                                         20-DEC-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-572016/53.
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Best Local Similarity
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9, Appli 8, Appli 2, Appli 8, Appli 8, Appli 13, Appli 13, Appl

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence S

Sequence

15, 15, 1, 1, 9, 1

Sequence Sequence Sequence Sequence

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1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09348953
; Patent No. 6538103
; Patent No. 6538103
; Patent No. 6538103
; APPLICANT: Information:
; APPLICANT: Trail, Pamela A.
; TITLE OF INVENTION: LYSINE BINDING FRAGMENTS OF ANGIOSTATIN
; TITLE OF INVENTION: LYSINE BINDING FRAGMENTS OF ANGIOSTATIN
; FILE REFERENCE: DB11Sequences
; CURRENT FILING DATE: 1999-07-07
; PRIOR PPLICATION NUMBER: 05/092,831
; PRIOR PLICATION NUMBER: 05/092,831
; ROTOR PRINCE DRIOR DATE: 1998-07-14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2: 8
; LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08612788
; Patent No. 5837682
; GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
; APPLICANT: Co. Tihai
; APPLICANT: Cao, Tihai
; APPLICANT: Cao, Tihai
; APPLICANT: APPLICANT: Anglostatin Fragments and Method of Use
; TITLE OF INVENTION: Anglostatin Fragments and Method of Use
; CORRESPONDENCE: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew
; STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%; Score 430; DB 4; Length 84;
83.3%; Pred. No. 1.1e-41;
ive 6; Mismatches 8; Indels
US-08-612-788-15
US-09-366-028-15
US-09-348-9515-15
US-09-348-9515-15
US-09-348-9515-15
US-09-35-25-9
US-09-35-25-9
US-09-35-325-9
US-09-35-325-9
US-09-35-325-9
US-09-35-325-13
US-09-35-325-13
US-09-35-325-13
US-09-35-325-13
US-09-335-325-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GPWCFTTDPSIRWEYCNLTRCSDT 84
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    Similarity
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CITY: Atlanta
STATE: Georgia
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Matches 7
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Sequence 23, Appli
Sequence 5, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 22, Appli
Sequence 22, Appli
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Sequence 21, App
                                                                                                                                     8; Search time 28 Seconds (without alignments) 134.488 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19,
Sequence 19,
Sequence 19,
Sequence 21,
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Sequence
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                                                                                                                                                                                                                                         523
1 VRQCYHGNGQSXRGTESTTV......SIRWEYCNLIRCSDIEGTVV
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                    5.1.6
Compugen Ltd.
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US-08-662-788-22
US-09-335-325-22
US-09-335-325-17
US-09-066-028-17
US-09-066-028-17
US-08-09-066-028-17
US-09-066-028-20
US-09-066-028-20
US-09-066-028-18
US-09-335-325-18
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US-09-335-325-16
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                                                                                                                                                                                                                                                                                                                                                                328717 seqs, 42310858 residues
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                    GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                         September 29, 2003, 08:32:08
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                     US-10-088-548-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length I
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 89
                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                    protein
                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
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20011111111111008
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9 9

Use

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E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
TELEPHOX: 404-818-3799
                                                            05940-0251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                NAME: Warreh, William L.
REGIETRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 0594(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3709
TELEPRA: 404-818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CFTTDPSVRWEYCNLKKC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CFITDPSIRWEYCNLTRC 81
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   78 amino acids
                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 191 Peach
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-066-028-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08763528A
Patent No. 565421
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.7%; Score 417; DB 2; Length 78; 85.9%; Pred. No. 3.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMENE: PATENTIN RCLEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/763,528A
FILING.DATE: 12-DEC 1996
CLASSIFICATION: 530
          ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                            ATTORNEY ACENT INFORMATION:
NAME: Warren, William L.
REGISTARION NUMBER: 36,714
REFRENCE, DOCKET WINBER: 05213-0126
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CFTTDPSVRWEYCNLKKC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: K4
US-08-612-788-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 85.9
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO FRAGMENT TYPE: N ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-763-528A-5
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1 CYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRQKTPENYPNAGLTMNYCRNPDADKGPW 60
                                                                                                                                                                                                                                                                     4 CYHGNGQSYRGIFSITVIGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADIGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: FOLKMan, M. Judah
APPLICANT: Co'Reilly, Micheal
APPLICANT: Co', Tilhai
APPLICANT: So', Tilhai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                           Query Match 79.7%; Score 417; DB 2; Length 78; Best Local Similarity 85.9%; Pred. No. 3.1e-40; Matches 67; Conservative 5; Mismatches 6; Indels
; LOCATION: 1..78
; OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
US-08-763-528A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READALLS FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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0; Gaps

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GENERAL INFORMATION:
APPLICANT: FOLKMEN, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: O'N. Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     Length 78;
                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                 / Match 79.7%; Score 417; DB 4; Local Similarity 85.9%; Pred. No. 3.1e-40; nes 67; Conservative 5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-335-325-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGRATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/COCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08612788
Patent No. 5837682
                                                                                ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                              61 CFTTDPSVRWEYCNLKKC 78
                                                                                                                                                                                                                                                                                                                                                              64 CFTIDPSIRWEYCNLTRC 81
                      ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 78 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                         CLONE: K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: 1
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-612-788-22
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                                                                                                                                                                                                     Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FOLKman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: U.S.

ZIP: 30303-1769

COMPUTE: TOORS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                              Query Match 79.7%; Score 417; DB 3; Length 78; Best Local Similarity 85.9%; Pred. No. 3.1e-40; Matches 67; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA.

APPLICATION NUMBER: US/08/612,788
FILLING DATE: -UDKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 23, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CFTTDPSVRWEYCNLKKC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CFTTDPSIRWEYCNLTRC 81
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                         : 78 amino acids amino acid
                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                          8
                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                           ; CLONE: K4
US-09-066-028-23
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US-09-335-325-23
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4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCE: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SISTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: GUNCOWN-
PRIOR APPLICATION UNBER: US/08/612,788
FILING DATE: GUNCOWN-
ATTORNEY/AGENT INFORMATION:
NAME: WATEN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 22: US-09-335-325-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
                         64 CFIIDPSIRWEYCNLIRC 81
                                               64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 404-818-3799
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FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: K4
                                                                                                                                                   US-09-335-325-22
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                                                                                                          1 CYQSDGQSYRGISSTIIIGKKCQSWAAMFPHRHSKIPENFPDAGLEMNYCRNPDGDKGFW 60
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                                               0; Gaps
                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09066028
Patent No. 6024688
Patent No. 6024689
Patent O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
70.6%; Score 369; DB 2; Length 78; 73.1%; Pred. No. 8.6e-35; ive 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.6%; Score 369; DB 3; Length 78; Best Local Similarity 73.1%; Pred. No. 8.6e-35; Matches 57; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REPERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                          64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACIERISTICS:
                   73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                             57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georgia
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CLONE: K4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                        RESULT 7
US-09-066-028-22
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  Query Match
                                           Matches
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61 CYTTDSQLRWEYCEIPSC 78
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                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 78 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Murine
                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: K3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-335-325-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                      Patent No. 555,000
GENERAL INFORMATION:
APPLICANT: FOlkman, M. Judah
APPLICANT: Cao, Yilhai
APPLICANT: Cao, Yilhai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sin, B. Kim Lee
TILLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.8%; Score 313; DB 2; Length 78; Best Local Similarity 61.5%; Pred. No. 1.9e-28; Matches 48; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788 FILING DATE:
                                                                                                                                                                                                                           E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNETY AGENT INFORMATION:
NAME: WATTEN, William L.
REGISTRATION NUMBER: 36,714
REPRENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3709
TELEPHONE: 404-818-3799
INFORMATION FOR SED ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             CITY: Atlanta
CONTRY: Atlanta
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: Bub PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6024688
GENERAL INFORMATION:
                                ; Sequence 17, Application US/08612788
; Patent No. 5837682
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61 CYTTDSQLRWEYCEIPSC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRACKERT TYPE: No CERMINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Murine; IMMEDIATE SOURCE: CLOME: K3 US-08-612-788-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 78 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: N
ANTI-SENSE: NO
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                US-08-612-788-17
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1 CLKGRGENYRGIVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNPDGETAPW 60
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Patent No. 6521439
GENERAL INFORMATION:
CENTRAL INFORMATION:
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
FITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Alanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PRIORPY disk
COMPUTER: PRIORD SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentION Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 59.8%; Score 313; DB 3; Best Local Similarity 61.5%; Pred. No. 1.9e-28; Matches 48; Conservative 9; Mismatches 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren, William L.
REGIETRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213
TELECOMAUNICATION INPORMATION:
TELEFROUE: 404-818-3700
TELEFRY: 444-818-3799
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
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61 CYTTDSEVRWDYCKIPSC 78
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NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Porcine
) IMMEDIATE SOURCE:
CLONE: K3
US-08-612-788-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.
ZIP: 30303-1769
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US-09-066-028-20
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Patent No. 5837682
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Xim Lee
TILE OF INVENTON: Angiostatin Fragments and Method of Use
                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325

FILING DATE: 17-Jun-1999

CLASSIFFICATION NUMBER: US/08/612,788

APPLICATION NUMBER: US/08/612,788

APPLICATION NUMBER: US/08/612,788

TILING DATE: TONNOWNDATA:

APPLICATION NUMBER: US/08/612,788

FILING DATE: TUNNOWNDATA:

APPLICATION NUMBER: US/08/612,788

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 05213-0126

TELEPRONE: 404-818-3799

INFORMATION FOR SEQ ID NO: 17:

SERUBECE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 59.8%; Score.313; DB 4; Length 78; Best Local Similarity 61.5%; Pred. No. 1.9e-28; Matches 48; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                   COMPUTER READABLE FORM:
MBDIUM TYPE: FLOPPY disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: K3
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 78 amino acids
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61 CYTTDSQLRWEYCEIPSC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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US-08-612-788-20
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4 CYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADIGPW 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: Cao, Nichally, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
CORRESPONDENCE ADDRESS: 45
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 57.2%; Score 299; DB 2; Length 78; l Similarity 56.4%; Pred. No. 7.4e-27; 44; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
APPLICATION:
FILING DATE:
CLASSIFICATION: 514
APTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
FELEPAX: 404-818-3709
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TELNGTH: 78 amino acids
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FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 44; Conservat
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                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
TELEFAX: 4
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US-08-612-788-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CYHGNGQSYRGIFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMMYCRNPDADIGFW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
CITY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
10.5.
2 IP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATA:
APPLICATION NUMBER: WS/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION NUMBER: WS/08/612,788
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: WS/08/612,788
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: 36,714
REGISTRATION NUMBER: 36,714
REFERRENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 57.2%; Score 299; DB 3; Length 78; 1 Similarity 56.4%; Pred. No. 7.4e-27; 44; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
  05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
                TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPAX: 404-818-3700
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
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61 CYTIDSEVRWDYCKIPSC 78
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INFORMATION FOR SEQ ID NO: 20:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                              ); ORGANISM: Porcine
); IMMEDIATE SOURCE:
); CLONE: K3
US-09-066-028-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                    TYPE: amino & STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-335-325-20
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4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW
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APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Ca'y Yihai
APPLICANT: Ca'y Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
                                                                                                                                                                                                                                                                                                                              ch 57.2%; Score 299; DB 4; Length 78; 1 Similarity 56.4%; Pred. No. 7.4e-27; 44; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Georgia

STATE: Georgia

COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CTASCETTON
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191 Peachtree Street, 37th Floor
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ATTORNEY/AGENT INFORMATION:
NAME: WALTEN, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET WIMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                     ; CLONE: K3
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-335-325-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/08612788 Patent No. 5837682
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||| :||:|| : |
61 CYTIDSEVRWDYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CFITDPSIRWEYCNLTRC 81
                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Porcine IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 18:
                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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; IMMEDIATE SOURCE: ; CLONE: K3 US-08-612-788-18
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ó 0; Gaps Query Match 54.5%; Score 285; DB 2; Length 78; Best Local Similarity 55.1%; Pred. No. 2.8e-25; Matches 43; Conservative 10; Mismatches 25; Indels Qγ Dp

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Search completed: September 29, 2003, 08:37:06 Job time : 29 secs

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September 29, 2003, 08:35:54 ; Search time 61 Seconds (without alignments) 220.760 Million cell updates/sec
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1 VRQCYHGNGQSYRGTFSTTV.....SIRWEYCNLTRCSDIEGTVV
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566894 seqs, 151307093 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                             US-10-088-548-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 89
                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                             Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COMPUTER: IBM PC_compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30

MEDIUM TYPE: Floppy disk

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,064
FILING DATE: 29-Dec-2000
CLASSIFCATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/763,528
FILING DATE: 12-DEC-1996
ATTORNEY/AGENT INPORMATION:

NAME: Warren, William L. REGISTRATION NUMBER: 36,714 REFERENCE/DOCKET NUMBER: 05940-0251

TELECOMMUNICATION INFORMATION: TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:

Description	Sequence 5, Appli Sequence 23, Appl Sequence 23, Appl Sequence 9, Appli Sequence 9, Appli		Sequence 17, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 18, Appl
SUMMARIES ID	US-09-753-064-5 US-09-761-120-23 US-09-335-325-23 US-10-267-137-9	US-09-761-120-22 US-09-335-325-22 US-10-131-241-22 US-09-761-120-17 US-09-335-325-17	US-10-131-241-17 US-09-761-120-20 US-09-335-325-20 US-10-131-241-20 US-09-335-325-18
DB	9 0 1 1 2 1 2 2 1 5 1 5 1 5 1	101101	15 10 10 10
% Query Match Length DB	78 778 778 788 788 788 788 788 788 788	7 7 7 8 8 8 7 7 8 8 8 8 8 8 8 8 8 8 8 8	78 78 78 78
% Query Match	79.7 79.7 79.7 79.7	70.07	59.8 57.2 57.2 57.2
Score	4 4 4 1 7 7 4 4 4 1 7 7 4 1 7 7 1 7 1 7	369 369 313 313	313 299 299 285
Result No.	H 40 W 4 L	1008760	11 12 14 15

1 412 1 6	Sequence 2, Sequence 2, Sequence 8, Sequence 7, Sequence 7, Sequence 14, Sequence 14, Sequence 14, Sequence 1, Seq	Cell Proliferation Inhibitor f Use LP t, 37th Floor
US-09-76 US-09-76 US-09-76 US-09-76 US-09-76 US-09-76 US-09-76 US-09-76 US-09-76 US-10-13 US-10-13 US-10-13 US-10-13 US-10-13 US-10-13	US-10-131-2 US-09-753-06 US-09-751-12 US-09-35-35-31 US-10-131-2 US-09-761-12 US-09-761-12 US-09-761-12 US-09-761-12 US-09-761-12 US-09-761-12 US-09-761-12	ial od o w, I tree
		S/0975 1 hai hai hai m. J Endo and S: 6 S: 6 eachtr eachtr FORM:
7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	77777777777777777777777777777777777777	Application US/09753064 US20010016644A1 INFORMATION: ICANT: Cao, Yihai E OF INVENTION: Endothel E OF INVENTION: Endothel ERRORE SEQUENCES: 6 ERRORDENCE ADDRESS: ADDRESSE: J01 Peachtree STREET: 191 Peachtree STREET: Atlanta STREET: 44 Anta
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4444444	-064-5 No. US20010016644A AL INFORMATION: APLICANT: Cao, Yi ROLMANT TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPENCE JOL STREET: 191 P CITY: ALIANT STABE: Georgi COUNTRY: US ZIP: 33033 COMPUTER: READABLE WATHER READABLE
2833 2833 2833 2831 2811 2811 2817 2777 2777 2775 2775 2775 2775 2775 27	2009 2009 2009 2009 2009 2009 4009 4009	164- 5, U 1 IN PLLI TLE RRE
11110000000000000000000000000000000000	U W W W W W W A A A A A A A A A A A A A	RESULT 1 US-09-753-C Sequence Patent NG GENERAL TI TI TI CCC CCC
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4 CYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Reilly, Micheal
Cao, Yihai
Sim, Br Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                               Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhoù, Qing-wei APPLICANT: Xb. Ren
TITLE OF INVERYION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
TITLE OF INVERYION: GROWTH FACTOR AND USES THEREFOR
                                                                                                              ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.7%; Score 417; DB 10;
85.9%; Pred. No. 5.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                      COUNTRY: U.S.
21P: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 9, Application US/10267137; Publication No. US20030148950A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CFTTDPSVRWEYCNLKKC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Conservative
                                                                                                                                                    CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xin, Li
APPLICANT: Li, Zai-Ping
APPLICANT: Gan, Ren-bao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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Sequence 23, Application US/09761120

Patent No. US20020037847A1

GENERAL INFORMATION:
APPLICANT: POLYMEND.
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
FILE REFERENCE: 05940-0151 (4311-252068)
CURRENT APPLICATION NUMBER: US/09/761,120

CURRENT APPLICATION NUMBER: US/09/761,120

CURRENT APPLICATION NUMBER: 09/309,821

PRIOR APPLICATION NUMBER: 08/866,735

PRIOR FILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.0

SEQ ID NO 23

LENGHH: 78

LENGHH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CYHGNGQSYRGTFSTIVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADIGPW 63
                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                             .;0
                                                                                                                                                                                          LOCATION: 1..78
OTHER INFORMATION: /note= "Kringle 4 - Figure 3"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.7%; Score 417; DB 9; Length 78; 85.9%; Pred. No. 5.6e-39;
                                                                                                                                                                                                                                                                                   ch 79.7%; Score 417; DB 9; Length 78; 1 Similarity 85.9%; Pred. No. 5.6e-39; 67; Conservative 5; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 23, Application US/0935325
; Patent No. US20020164717A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 CFTTDPSIRWEYCNLTRC 81
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                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Kringle 4
                                                                                                                                                                      NAME/KEY: Protein
                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 67; Conserv
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US-09-761-120-23
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APPLICANT: O'Really, Michael
TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmil
FILE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmil
FILE REPERENCE: 05940-0151 (43171-252068)
CURRENT PELLON UNDER: 05/09/761,120
CURRENT FILING DATE: 1209-05-11
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR APPLICATION NUMBER: 09/866,735
PRIOR FILING DATE: 1999-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CYQSDGQSTRGTSSTTITGKKCQSWAAMFPHRHSKTPENFPDAGLEMNYCRNPDGDKGPW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CYHGNGQSYRGIFSTTVTGRTCQSWSSMTPHRHQRIPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.6%; Score 369; DB 9; Length 78; Best Local Similarity 73.1%; Pred. No. 1.2e-33; Matches 57; Conservative 10; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta STATE: Georgia COUNTRY: U.S.

ZIP: 30303-1768
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/612,788
FILING DATE: CURNOWN>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
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TELEFAX: 404-818-3799
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 4
US-09-761-120-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Murinae gen. sp.
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US-10-131-241-23

Sequence 23, Application US/10131241

Publication No. US20030012792A1

GENERAL IMPORATION: US20030012792A1

APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT PILING DATE: 1999-00-22

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

PRIOR PILING DATE: 1999-05-22

NUMBER: OF SEQ ID NOS: 65

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 23

LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                               Score 417; DB 12; Length 78;
Pred. No. 5.6e-39;
5; Mismatches 6; Indels
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Pred. No. 5.6e-39;
                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Sequence alignment of kringle domains of ... OTHER INFORMATION: plasminogen and HGF US-10-267-137-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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                CURRENT APPLICATION NUMBER: US/10/267,137
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/328,329
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                  79.78;
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                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FILE REFERENCE: 524282000100
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Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-241-23
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Best Local Similarity
Matches 67; Conserv
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US-09-761-120-22
                                                                                                                                         SEQ ID NO 9
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TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: 08/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Version 3.0
ENGINE FILING DATE: 1997-05-30
SOFTWARE: Patentin Version 3.0
ENGINE OF SEQ ID NOS: 47
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US-03-335-325-17
US-09-335-325-17
Sequence 17, Application US/09335325
Sequence 17, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
Cao, Yihai
Sim, B. Kim Lee
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM
COMPUTER: TIPE FLORMY GISK
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COMPUTER: TIPE FLORMY GISK
COMPUTER: TIPE FLORMY FREIGHTON DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: TOWN CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
CLASSIFICATION: CURROWN>
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CLASSIFICATION CURROWN>
CLASSIFICATION DATA:
COMPUTER: TIPE CANAME COMPUTER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.8%; Score 313; DB 9; Length 78; Best Local Similarity 61.5%; Pred. No. 1.9e-27; Matches 48; Conservative 9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren, William L.
REGIGSTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 404-818-3700
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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61 CYTIDSQLRWEYCEIPSC 78
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                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAMB/KEY: misc_feature
CTHER INFORMATION: Kringle 3
US-09-761-120-17
APPLICANT: O'Reilly, Michael
                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Murinae gen. sp.
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APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

TITLE DE INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CORRENT RPLICATION NUMBER: US 09/10/131,241

CORRENT FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1998-05-21

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOCTWARE: Patentin version 3.1

SEQ ID NO 22

LENGTH: 78

LENGTH: 78
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                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                    TYPE: amino acid
STRANDENESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 22, Application US/10131241; Publication No. US20030012792A1; GENERAL INFORMATION:
LENGTH: 78 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 CFITDPSIRWEYCNLTRC 81
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                                                                                                                                                                                                                          ORGANISM: Murine
                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Murinae sp. US-10-131-241-22
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Matches 57; Conserv
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US-09-761-120-17
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US-10-131-241-22
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TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasmin FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: 05/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Petentin version 3.0
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                  4 CYHGNGQSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMMYCRNPDADIGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                     O'REILLY, Micheal
Cao, Yihai
Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           Length 78;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FLING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUWRRY: U.S.
ZIP: 30303-1769
COMPUTER READBLE FORM:
                                                                                                                                                                                                                                                                                                                                           ; Score 299; DB 9;
; Pred. No. 6.9e-26;
12; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 05213-0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
FILING DATE: «UDKNOWD»
AITORNEY/AGENT INFORMATION:

NAME: WARTEN, William L.

REGISTRATION NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 20, Application US/09335325
; Patent No. US20020164717A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Folkman, M. Judah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 78 amino acids TYPE: amino acid
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61 CYTTDSEVRWDYCKIPSC 78
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.4%;
Matches 44; Conservative 1:
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                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; OTHER INFORMATION: Kringle 3
US-09-761-120-20
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Sus sp.
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US-09-335-325-20
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                                                                                                                                                                                                                                                    Score 313; DB 10; Length 78;
Pred. No. 1.9e-27;
9; Mismatches 21; Indels
                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-335-325-17
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Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
APPLICANT: O'Reilly, Michael
                  STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                               61 CYTTDSQLRWEYCEIPSC 78
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                                                                                         ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                  ch 59.8%;
1 Similarity 61.5%;
48; Conservative 5
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Best Local Similarity 61.55
Matches 48; Conservative
                                                                                                                                             ORGANISM: Murine
IMMEDIATE SOURCE:
                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                   CLONE: K3
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ORGANISM: Murine
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US-09-761-120-20
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US-10-131-241-17
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Best Local Si
Matches 48;
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4 CYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW
Sim, B. Kim Lee TITLE OF INVENTION: Angiostatin Fragments and Method of Use NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                          CITY: Atlanta
STATE: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
COUNTRY: Atlanta
CONFORTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUBBR: US/09/335,325
FILIGATION NUBBR: US/09/335,325
FILIGATION NUBBR: US/09/335,325
FILICATION NUBBR: US/09/335,325
FILICATION NUBBR: US/08/612,788
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                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 29, 2003, 08:45:29
Job time : 62 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 78 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: K3
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Sequence 20, Application US/10131241

Publication No. US20030012792A1

Sequence 20, Application No. US20030012792A1

Sequence 20, Application No. US20030012792A1

SEQUENCE INFORMATION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: ANDRER: US/10/131,241

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-10-06

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 65

SEQ ID NO SEQ ID NOS: 65

LENGTH: 78

LENGTH: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CYHGNGQSYRGTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                        Length 78;
                                                                                                                                                                                                                                                                                                                                                                           22; Indels
                                                                                                                                                                                                                                                                                                                     57.2%; Score 299; DB 10; 56.4%; Pred. No. 6.9e-26; tive 12; Mismatches 22;
                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09335325
Patent No. US20020164717A1
GENERAL INFORMATION:
APPLICANT: FOlkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||| :||:|| : |
61 CYTIDSEVRWDYCKIPSC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 CFTTDPSIRWEYCNLTRC 81
                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                        ORGANISM: Porcine IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 56.4%
Matches 44; Conservative
                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Porcine US-10-131-241-20
                                                                                                                                                                                                                                                                       US-09-335-325-20
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US-09-335-325-18
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 29, 2003, 08:30:58; Search time 39 Seconds (without alignments) 219.462 Million cell updates/sec Run on:

US-10-088-548-6 523 1 VRQCYHGNGQSYRGTFSTTV.....SIRWEYCNLTRCSDTEGTVV Title: Perfect score: Sequence:

Scoring table:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

30955

Minimum DB seq length: 0 Maximum DB seq length: 89

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Dlasmin (EC 3.4.2)	short neurotoxin -	short neurotoxin 2	Ig kappa chain - m	hypothetical prote	intestinal trefoil	kappa-3 neurotoxin	proteinase inhibit	hypothetical prote	H+-transporting tw	capsid gene 5'-reg	high-potential iro	conserved hypothet	pS2 protein precur	hypothetical prote	short neurotoxin 1	NADH2 dehydrogenas	hypothetical prote	protein T22C5.7 [i	hypothetical prote	intestinal trefoil	protease inhibitor	hypothetical prote	mambin - eastern J	short neurotoxin 1	short neurotoxin 1	short neurotoxin 1	hypothetical prote	envelope protein -
	Ωī	A60140	0300%	NIRIZ	824216	T34687	A41441	B60549	T14395	S41030	E58892	\$23703	841611	AC0142	A26667	G69176	NIEYI	T11380	AF0060	D86401	T14930	S23963	S30578	S63324	TGEP5J	NIATI	NIATIF	A27580	E82747	S35815
	DB		~	1	7	7	7	N	7	7	~	~	7	N	~	C4	Н	7	7	(1	7	~	7	~	Н	Н	Н	7	~	7
	Query Match Length	68	64	61	67	16	81	87	77	88	52	82	72	81	84	82	9	79	73	77	77	80	77	52	59	09	09	9	64	77
ф (Query Match	67.7	12.2	11.8	10.3	9.0	-:	9.0	9.5	9.5	9.4	9.4	9.3	•	9.1	9.1	0.6			8.8	ω	8.8		8.6			٠	8.0		
	Score	354	64	61.5	54	25	52	20	a,	49.5	49	4.9	48	48	47.5	47.5	47	46.5	46	46	46	46	45.5	45	45	45	45	45	45	45
·	Resurt No.		(7)	m	4	2	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	- 29

long neurotoxin 2 fibrinogen receptor	short neurotoxin I	hypothetical prote hynothetical prote	short neurotoxin 1	hypothetical prote	ribosomal protein	very hypothetical	short neurotoxin c	hypothetical prote	proteinase inhibit	insect toxin I5 -	toxin-like protein	short neurotoxin A	Ig kappa chain V r
N1KF2U A54369	B25866	T17765 T3/975	NIRII	D81915	G69136	T35239	F25866	T31295	B84433	JN0361	S06667	NIAY1	S26474
п С	7	~ ~	٧	~	~	7	~	7	~	7	7	Н	7
87 60	62	71	0.0 0.0	29	88	54	62	74	77	35	35	9	68
 9.0.				8.4	8.4	8.3	8.3	8,3	8.3		8.3	8.2	8.3
	8			44 8.4	44 8.4	43.5 8.3		43.5 8.3	43.5 8.3		æ	43 8.2	43 8.2

ALIGNMENTS

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plasmin (EC 3.4.21.7) precursor - chicken (fragment)
Nalternate names: plasminogen
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Bete: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C.Accession: A60140
R.Gyenes, M.; Patthy, L.
B.cohim. B.tophys. Acta 832, 326-330, 1985
A.Title: The Kringle 4 domain of chicken plasminogen.
A.Reference number: A60140; MUID:86077796; PMID:4074753
A.Residues: 1-89 GGIES
A.Residues: 1-89 GGIES
C.Reywords: fibrinolysis: glycoprotein; hydrolase; kringle; plasmis; serine proteinas:
F.6-83/Domain: kringle homology cracked
F.50-Fibrinolys Assultate bonds: #status predicted
F.39/Einding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ECYQGNGVSYRGTASFTIIGKKCQAWNSMSPHRHNKTESHFPNADLRQNYCRNPDADRSP
5 ECYQGNGVSYRGTASFTIIGKKCQAWNSMSPHRHNKTESHFPNADLRQNYCRNPDADRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLIMNYCRNPDADTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.7%; Score 354; DB 2; Length 89; Best Local Similarity 67.9%; Pred. No. 2.1e-29; Matches 55; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 WCFTTDPSIRWEYCNLTRCSD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 WCYTTDPSVRWEYCNLKRCSD
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Short neurotoxin - banded krait
C.Species: Bungarus fasciatus (banded krait)
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
C.Backession: JX0060
R.Liu, C.S.; Chen, J.P.; Chang, C.S.; Lo, T.B.
J. Biochem. 105, 93-97, 1989
J. Title: Amino acid sequence of a short chain neurotoxin from the venom of banded krizherence number: JX0060; MUID:89291813; PMID:2738048
A.Reference number: JX0060
A.Residues: 1-64 -LIUD
C.Superfamily: snake toxin
C.Superfamily: snake toxin
C.Superfamily: snake toxin

ä Gaps 10; 12.2%; Score 64; DB 2; Length 64; llarity 26.7%; Pred. No. 7.2; Conservative 7; Mismatches 27; Indels Query Match Best Local Similarity Matches 16; Conserva

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NAlternate names: Kappa-3 bungarofoxin; Kappa-neurotoxin CR1
(Species: Bungarus multicinctus (many-banded krait)
(Joate: 17-Apr-1993 #sequence_revision 18-Jun-1993 #text_change 17-Mar-2000
(Sacession: 508398; B60549
(R.Danse, J.M.; Garnier, J.M.)
(Notelac Acids Res: 18, 1050, 1990
(A) Title: cDNA deduced amino-acid sequences of two novel Kappa-neurotoxins from Bungar A) Reference number: 508398; MoID:90192091; PMID:2315018
(A) Residues: 1-87 CADAN
(A) Residues: 1-87 CDAN
(A) Residues: 1-87 CDAN
(A) Residues: EMBL:X51413; NID:962481; FIDN:CAA35775.1; PID:962482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAA18983.1; GSPDB:GN00070; SCOEDB:SC1B5.09c
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                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                            HGHDREPE----PDGAGCEPGGYCLIDAPRPPKADGPPFAECVOCKEPTEYPESYKGITLC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intestinal trefoil factor precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: mRNA
A.Residues: 1-81 <SUE>
A.Cross-references: GB:M80826; NID:g207446; PIDN:AAA42270.1; PID:g207447
A.Note: the authors translated the codon ACA for residue 8 as Ile
C.Superfamily: secretory protein xP1; trefoil homology
C.Reywords: intestine
F):1-20/Domain: signal sequence #status predicted <SIG>F:1-22/Domain: propeptide #status predicted <PRO>
F:21-22/Domain: propeptide #status predicted <ARD>
F:23-81/Product: intestinal trefoil factor #status predicted <AAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 FSTT-----VTGRTC--QSWSSMTPHR-----HQRTPENYPNDGLTMNYCRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.9%; Score 52; DB 2; Length 81; Best Local Similarity 28.2%; Pred. No. 1.5e+02; Matches 20; Conservative 8; Mismatches 17; Indels
                                                                                                                                                                                                                                             Length 76;
                                                                                                                                                                                                                                                                                                                                                        34 HRHQRTPENYPNDGLTM---NYC----RNPDADTGPWC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;33-73/Domain: trefoil homology <TRF>
F;33-59,43-58,53-70/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                9.9%; Score 52; DB 2; 27.0%; Pred. No. 1.5e+02;
                    A, Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
A; Residues: 1-76 < HAR>
A; Residues: 1-76 < HAR>
A; Cross-references: EMBL; AL023517; PIDN: CAA18983.1; A; Experimental source: strain A3(2)
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kappa-3 neurotoxin precursor - many-banded krait
                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 PVCEWQEAQRIACS 75
                                                                                                                                                                                                                                                                       Best Local Similarity 27.0 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PSIRWEYCNLTRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 -PDADTGPWCF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IPNV---PWCF
                                                                                                                                                                                         A; Gene: SCOEDB: SC1B5.09c
A; Accession: T34687
                                                                                                                                                                                                                                                                                                                                                                                                               n
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                          Short neurotoxin 2 - ringhals
NyAlternate names: neurotoxin 1V
C;Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C;Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C;Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
C;Species: Ja.out.1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C;Accession. AOITO: Bortes, D.P.
J. Biol. Chem. 246, 1341-1349, 1971
A;Hitle: Snake venom toxins. Purification, properties, and complete amino acid sequence A;Reference number: A92073; MuID:71116407; PMID:5545078
A;Reference number: A92073; MuID:71116407; PMID:5545078
C;Superfamily: snake toxin
C;Seywords: neurotoxin; venom
C;Seywords: neurotoxin; venom
C;Seywords: neurotoxin; venom
F;3-23,17-40,42-53,54-59/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain - mouse (fragment)
C)species: Mus musculus (house mouse)
C)species: Mus musculus (house mouse)
C)ate: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: $24216
R;Shhnitau, T: Ivasato, T:; Yamagishi, H.
B;Shhnitau, T: Ivasato, T:; Yamagishi, H.
A;Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excis
A;Reference unber: $24214; MUID:91217618; PMID:1902500
A;Status: preliminary; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QCYHGNGQSYRGTFSTTVTGRTC-----QSWSSMTPHRHQRTPENYPNDGLTMNYCR 54
                          HRHQRIPENYPNDG------LTMNYCRNPDADIGFWCFTTDPSIRWEYCNLTRCSD 83
                                                       hypothetical protein SC1B5.09c SC1B5.09c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-67 <SHI>
A; Cross-references: EMBL:X58221; NID:953719; PIDN:CAA41185.1; PID:9930196
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1998
A; Reference number: 22187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 2; Length 67; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VRQCYHGNGQSYRGTPS----TTVTGRTCQSWSSMTPH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 VRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.5; 1
Pred, No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ERGCGCPTVKPGIKLKCCTTDRCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 NPDADJGPWCFTTDPSIRWEYCNLTRCS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.3%;
39.5%;
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Best Local Similarity 39.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Conservative
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Best Local Similarity
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown; not o A; Molecule type: DNA
A; Residues: 1-55 <2AR>
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                                                                                                                                                                                                                                                                                                                                                        Rizardoya, R.; Meyer, A. Genetics 146, 995-1010, 1997
Genetics 146, 995-1010, 1997
A; Fitler The complete DNA sequence of the mitochondrial genome of a "living fossil,"
A; Reference number: A58892; MUID:97358858; PMID:9215903
A; Accession: E58892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: FOR7944-8111
A;Genome: mitochondrion
A;Genome: mitochondrion
C;Guperfamily: H+-transporting AIP synthase protein 8
C;Keywords: AIP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                   H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - coelacanth mitochondrion C;Species: mitochondrion Latimeria chalumnae (coelacanth) C;Date: 30-Oct-1998 #sequence_revision 30-Oct-1998 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------WPRGLLNMKSCTLNPQHMLRLWIITTASSMAW 71
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high-potential iron sulfur protein isoform 1 - Ectothiorhodospira vacuolata
N'Alternate names: HIPIP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 TESTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCR-NPDADTGPWCFTTDPSIRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references; GB:U82228; NID:91916817; PIDN:AAC60322.1; PID:91916822 A;Note: submitted to GenBank/EMBL/DDBJ December, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Experimental source: strain F9
A;Note: submitted to the EMBL Data Library, November 1991
                         59
                                                           2 GOSPSSFNARQT-----SSSTPQKSTKTP-----TCSDPRSPSQD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                            GOSYRGIFSTIVIGRICQSWSSMIPHRHQRIPENYPNDGLIMNYCRNPDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.4%; Score 49; DB 2; Length 82;
ilarity 28.4%; Pred. No. 3.2e+02;
Conservative 3; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                % Match 9.4%; Score 49; DB 2; Length 55; Local Similarity 34.1%; Pred. No. 2.1e+02; nes 14; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 SW---SSMTPHRHQRTPENYPNDGLIMNYCR-NPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 SWLIFLTMLPSKTQL--HTFPNMPSTQNMCKQEPEPWTWPW 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: genomic RNA A; Residues: 1-82 <CA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 SFSTRFTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 EYCNLTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RR-GLIR 77
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                     C; Accession: E58892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ATPase8
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                  A;Title: Kappa-2-bungarotoxin and kappa-3-bungarotoxin: two new neuronal nicotinic recept A;Reference number: A60549; MUID:90213167; PMID:2322821
A;Accession: B60549
                                                                                                                                                    A;Molecule type: protein
A;Residues: 22-66 <CHI>
C;Comment: Kappa-3-neurotoxin exists as homodimers and as heterodimers with kappa-2-neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Kim, J.B.; Kim, H.U.; Yun, C.H.; Park, B.S.; Cho, W.S.; Ryu, J.C.; Chung, T.Y. submitted to the EMBL Data Library, March 1996
A,Description: Nucleotide sequences of protease inhibitor II in chinese cabbage. A,Reference number: 218029
A,Reference number: 218029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 RICQSWSSMIPHRHQRIPENYPN-----DGLIMNYC--RNPDADIGPWCFIIDPSIRW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteinase inhibitor II - turnip
C;Species: Brassica rapa (turnip)
C;Date: 20-5ep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein K03H1.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 *sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C;Accession: S41acough, R.
R;Smith, M.; Ainscough, R.
submitted to the EMBL Data Library, January 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 77;
                                                                                                                                                                                                                                         C;Superfamily: snake toxin
C;Keywords: heterodiner; honodiner; neurotoxin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-87/Product: Kappa-3-neurotoxin #status experimental <AAT>
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.6%; Score 50; DB 2; Length 87; Best Local Similarity 29.4%; Pred. No. 2.7e+02; Matches 20; Conservative 6; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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A;Molecule type: mRNA
A;Residues: 1-77 < KIM>
A;Torss-references: EMBL: L31937; NID:g1209257; PID:g1209258
A;Experimental source: unopened flower bud
C;Superfamily: gamma-thionin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 GMGPVTVEARTCESKS----HRFKGTCVSSINCG---NVCHN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRN 55
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R;Chiappinelli, V.A.; Wolf, K.M.; Grant, G.A.; Chen, S.J.
Brain Res. 509, 237-248, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 9.5%; Score 49.5; DB 2; Similarity 38.1%; Pred. No. 2.7e+02; 16; Conservative 3; Mismatches 16;
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A; Accession: $41030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 EYCNLTRC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 NYRSLLCC 80
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A; Residues: 1-88 <SMI>
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A, Molecule Type: protein
A, Residues: 25-60 <MO3>
K, Chadwick, M.P.; May, F.E.B.; Westley, B.R.
Biochem. J. 308, 1001-1007, 1995
A, Title: Production and comparison of mature single-domain 'trefoil' peptides pNR-2/p
A, Reference number: 556001; MUID:97104304; PMID:8948462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Accession: A56743
A)Molecule type: protein
A;Molecule type: protein
B;Jakowlew, S.B.; Breathnach, R.; Jeltsch, J.M.; Masiakowski, P.; Chambon, P.
Nucleic Acids Res. 12, 2861-2878, 1984
A;Title: Sequence of the pS2 mRNA induced by estrogen in the human breast cancer cell
A;Reference number: S11505; MUID:84169578; PMID:6324130
A;Accession: S11505.
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R; Mori, K.; Fujli, R.; Klda, N.; Ohta, M.; Hayashi, K.
Blochem. Blophys. Res. Commun. 155, 366-372, 1988
A; Title: Identification of a polypeptide secreted by human breast cancer cells (MCF-7 A; Reference number: A31573; MUID:88326327; PMID:3261981
A; Accession: A31573
                                                                                                                                                                                          A. Molecule type: protein
A. Residues: 25-35 <TA2>
A. Residues: 25-35 <TA2>
A. Residues: 25-35 <TA2>
J. Biochem. 107, 73-76, 1950
A. Hitle: Complete primary structure of the human estrogen-responsive gene (pS2) produ
A. Reference number: JXX0093; MUID:90236983; PMID:2185238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Nolecule type: mRNA
A;Residues: 1-84 <JAK>
K.cross-references: EMBL:X00474; NID:g35706; PIDN:CAA25155.1; PID:g35707
R;Prud'homme, J.F.; Fridlansky, F.; Le Cunff, M.; Atger, M.; Mercier-Bodart, C.; Pich
DNA 4, 11-21, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA 4, 11-21, 1985
A;Title: Cloning of a gene expressed in human breast cancer and regulated by estrogen
A;Reference number: A22093; MUID:85126393; PMID:3838275
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                                                                                                              A:Cross-references: EMBL:X52003; NID:g311379; PIDN:CAA36254.1; PID:g35718 A:Accession: A38028
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A, Molecule type: mRNA
A, Residues: 2-84 < PRO:
A, Cross-references: GB:M12075; NID:g182203; PIDN:AAA52402.1; PID:g182204
R;Rio, M.C.; Lepage, P.; Diemunsch, P.; Roitsch, C.; Chambon, P.
C. R. Acad. Soil. III 307, 825-831, 1988
A, Title: Primary structure of the human ps2 protein.
A;Reference number: S06457; MUID:89119134; PMID:3146413
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Pred. No. 4.6e+02;
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Best Local Similarity 31.0%;
Matches 18; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JX0093
A; Molecule type: mRNA
A; Residues: 1-84 <MOR>
                                               A; Molecule type: mRNA
A; Residues: 1-84 <TAK>
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0142
G;Accession: AC0142
A;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Atle: Genome sequence of Persinia pestis, the causative agent of plague.
A;Atcus: preliminary
A;Accession: AC0142
A;Status: preliminary
A;Accession: AC0142
A;Cose-references: GB:AL590842; PIDN:CAC89998.1; PID:g15979220; GSPDB:GN00175
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A,Residues: 1-84 <\pre>A,DEL
A,Residues: 1-84 <\pre>A,DEL
A,Cross: 1-84 <\pre>A,DEL
A,Cross: 1-84 <\pre>A,DEL
A,Cross: 1-84 <\pre>A,DEL:X05030; NID:g35712; FIDN:CAA28695.1; FID:g1246868; EMBL:X05321;
A,Experimental source: breast adenocarcinoma cell line NCF-7
R;Takahashi, H.; Kida, N.; Fujii, R.; Tanaka, K.I.; Ohta, M.; Mori, K.; Hayashi, K.
FEBS ictt. 2541, 283-286, 1990
A;Title: Expression of the pS2 gene in human gastric cancer cells derived from poorly di
A;Reference number: S08266; MUID:90184461; PMID:2311759
C; Species: Ectothiorhodospira vacuolata
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 13-Nov-1998
C; Accession: S41611
A; Mabler: R.P.; Weyer, T.E.; Kamen, M.D.
Arch. Blochem. Blophys. 308, 78-81, 1994
A; Title: Amino acid sequences of two high-potential iron sulfur proteins (HiPIPS) from A; Reference number: S41611; MUID:94145107; PMID:8311477
A; Recession: S41611
A; Molecule type: protein
A; Residues: 1-72 <AME>
A; Essidues: 1-72 <AME>
A; Essidues: 1-72 <AME>
A; Essidues: 1-72 <AME>
A; Esperimental source: strain beta 1; DSM 2111
C; Superfamily: high potential iron-sulfur protein; metalloprotein
C; Superfamily: high potential iron-sulfur protein; metalloprotein
F; 34, 37, 51, 65/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pS2 protein precursor - human N,Alternate names: estrogen-responsive gene pS2 protein; protein NR-2/pS2 (man) S,Abedies: Homo aspiens (man) C;Apedies: Homo aspiens (man) C;Date: 21-May-1888 #text_change 20-Jun-2000 C;Accession: A2667; 808260, A38028; JX0093; A56743; S11505; A22093; S06457; A31573; R;Jeltsch, J.M.; Roberts, M.; Schatz, C.; Garnier, J.M.; Brown, A.M.C.; Chambon, P. Muclaic Acids Res. 15, 1401-1414, 1997 A;Title: Structure of the human osetrogen-responsive gene pS2. A;Reference number: A26667; MUID:87146470; PMID:3822834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein YPO1157 [imported] - Yersinia pestis (strain C092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 QRTPE----NYPNDGLTMNYCRNPDADTGPWCFT----TDPS-IRWEYC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.2%; Score 48; DB 2; Length 72; 80.6%; Pred. No. 3.5e+02; lve 7; Mismatches 15; Indels
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40.6%; Pred. No. 4e+02;
tive 2; Mismatches
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Best Local Similarity 30.65
Matches 15; Conservative
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Best Local Similarity 40.6
Matches 13; Conservative
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RESULT 14

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RESULT 15
689176
hypothetical protein NTH58 - Methanobacterium thermoautotrophicum (strain Delta H)
c;Species: Methanobacterium thermoautotrophicum
c;Species: Methanobacterium thermoautotrophicum
c;Species: Ob-Dec-1999
C;Species: Ob-Dec-1999
C;Species: Methanobacterium thermoautotrophicum
c;Species: Methanobacterium thermoautotrophicum
c;Accession: G69176
R;Smith, D.R.: Doucette-Ztamm, L.A.; Deloughery, C; Lee, H; Dubois, J; Aldredge, T.;
c) Qlu, D. Spadafora, R; Vicaire, R; Mang, Y; Mierzbowski, J; Reeve, J; N.
d; S; Church, G.M.; Daniels, C.J.; Mao, J; Rice, P; Moelling, J; Reeve, J; N.
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H; funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; References: GB:AE000798; GB:AE000666; NID:92621094; PIDN:AAB84565.1; PID:9262109
A; Residues: 1-85 cARTH
A; References: GB:AE000798; GB:AE000666; NID:92621094; PIDN:AAB84565.1; PID:9262109
A; Residues: 1-85 cARTH
A; References: GB:AE000798; GB:AE000666; NID:92621094; PIDN:AAB84565.1; PID:9262109
A; References: GB:AE000798; GB:AE000666; NID:92621094; PIDN:AAB84565.1; PID:9262109
A; References: GB:AE000798; GB:AE000788; GB:AE000788;
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Search completed: September 29, 2003, 08:36:31 Job time: 41 secs sus scrofa bungarus mu

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homo sapien alnus gluti dendroaspis

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081701 P18328 P15222) P58548

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MEDLINE-89291813; PubMed-2738048; Liu C.-S., Chen J.-P., Chang C.-S., Lo T.-B.; Liu C.-S., Chen J.-P., Chang C.-S., Lo T.-B.; Anino acid sequence of a short chain neurotoxin from the venom of banded krait (Bungarus fasciatus)."; J. Biochem. 105:93-97(1989).

-i- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC ACETYLCHOLINE RECEPPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 HRHQRIPENYPNDG------LIMNYCRNPDADIGPWCFITDPSIRWEYCNLIRCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT: 64 AA.

P10808;
P101-1989 (Rel. 11, Created)
O1-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Bungarus fasciatus (Banded krait).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
PNCBL_TAXID=8613;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Postsynaptic neurotoxin; Multigene family.
26 BY SIMILARITY.
43 BY SIMILARITY.
56 BY SIMILARITY.
62 BY SIMILARITY.
7272 MW; 340A6AF40F5E06D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: Expressed by the venom gland.
-:- SIMILARITY: Belongs to the snake toxin family.
-:- SIMILARITY: Belongs to the snake toxin family.
-:- BYONGGO, JX0060.
-- HSSP; P01426; INEA.
-- INTERPRO; INEA.
-- INTERPRO; INEA.
-- INTERPRO; SNAKE_LOXIN; I.
-- PROSITE; PS00272; SNAKE_TOXIN; I.
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01, Last sequence update)
41, Last annotation update)
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Pred. No. 1.6;
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                                                                                                                         ALIGNMENTS
MCPI_HIRME
U2AG_PIG
NXL5_BUNMU
TX02_DENAN
NXSC_LATLA
NXL1_DENVI
NI9M_BOVIN
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SCX5_BUTEU
ME22_EUPRA
                                                             NI9M_HUMAN
                                                                    POC4_ALNGL
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Best Local Similarity 26.7
Matches 16; Conservative
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DISULFID 3
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64 AA;
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21-JUL-1986 (Rel.
28-FEB-2003 (Rel.
IISSUE=Venom;
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NXS2_HEMHA
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181.973 Million cell updates/sec
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                                                             September 29, 2003, 08:23:28; Search time 23 Seconds
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1 VRQCYHGNGQSYRGIFSTIV......SIRWBYCNLIRCSDIEGTVV
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                          127863 segs, 47026705 residues
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THG2_ARATH
CXMB_CONMR
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SCX3_MESTA
YSF1_RHILO
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NXL3_BUNMU
ATPB_LATCH
HPI1_ECTVA
TFF1_HUMAI
NXS1_ENHSC
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match
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83

Gaps

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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                          3 QCYHGNGQSYRGTFSTTVTGRTC-----QSWSSMTPHRHQRTPENYPNDGLTMNYCR 54
                                                                                                                                      J. Biol. Chem. 246:1341-1349(1971).
-1- FUNCTION: Produces peripheral paralysis by blocking neuromuscular transmission at the postsynaptic site. Binds to the nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Būkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Lamiales; Olesceae; Syringa.
NCBL_TaxID-34270;
                                                                                                                                                                                                MEDLINE-71116407; PubMed-5545078; Strydom A.J.C., Botes D.P.; Strydom A.J.C., Dates D.P.; Sand venom toxins. Purification, properties, and complete amino assake venom toxins. Purification Ringhals (Hemachatus haemachatus)
       Hemachatus haemachatus (Ringhals) (Sepedon haemachatus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria, Squamata; Scleroglossa; Serpentes; Colubroidea;
Blapidae; Blapinae; Hemachatus.
                                                                                                                                                                   acetylcholine receptor.
--- SUBCELLOIAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed by the venom gland.
---- MISCELLANDROUS: LD(50) is 0.09 mg/kg by intravenous injection.
--- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ledesma A., Villalba M., Rodriguez R.;
"Cloning and expression of a protein homologous to Ole e 3 from
Syringa vulgaris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Polcalcin Syr v 3 (Calcium-binding pollen allergen Syr v 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                55 NPDADTGPWCFTTDPSIRWEYCNLTRCS 82
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neurotoxin 2 (Toxin IV).
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P58171;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eur. J. Biochem. 258:454-459(1998).
-: SIMILARITY: Contains 2 EF-hand calcium-binding domains.
There are no restrictions on
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Lamiales; Oleacae; Olea.
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16-0CT-2001 (Rel. 40, Last annotation update)
Polcalcin Ole e 3 (Calcium-binding pollen allergen Ole e 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 YHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
9COC4A8BCE03B3FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
BC3B3DE011D409D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50.5; 1
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium-binding; Repeat; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pollen;
MEDLINE-99089607; PubMed-9874211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00054; EFh; 2.
PROSITE; PS00018; BF_HAND; 2.
Calcium-binding; Repeat; Allergen.
                                                                                                                                                                                                                              HSSP; P02588; IAVS.
InterPro; IPR002048; EF-hand.
Pfan; PF00036; efhand; 2.
ProDom; P0000012; EF-hand; 1.
SMART; SM00054; EFh; 2.
PROSITE; PS00018; EF_HAND; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF015810; AAD05375.1; -.
                                                                                                                                                                                                  EMBL; AF078681; AAK01144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA; 8994 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9356 MW;
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DB 1; Length 84;

Score 50.5;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensed(sb-sib.ch).
                                                     RICQSWSSMTPHRHQRTPENYPN-----DGLIMNYC--RNPDADIGPWCFITDPSIRW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zardoya R., Meyer A.;
Submitted (DEC-1966) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
(CF(0) SUBGNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Coelacanthiformes, Coelacanthidae, Latimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -! - CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001421; ATPase8_mit.
Pfam; PF00895; ATP-Synt_8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 4 24 DAMPHANEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
Ectothiorhodospiraceae; Ectothiorhodospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High potential iron-sulfur protein isozyme 1 (HiPIP 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 SW---SSMTPHRHQRTPENYPNDGLTMNYCR-NPDADTGPW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 SWLIFLTMLPSKTQL -- HTFPNMPSTQNMCKQEPEPWTWPW 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 24 POTENTIAL.
55 AA; 6569 MW; 7FE36319E8AF825B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #PIL_ECTVA STANK...

#PAIL_ECTVA STANK...

#PAIL_ECTVA

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56;
                                                                                                                                                                                                                                                                                                                                                                                                       мтатрв ок атрв.
Latimeria chalumnae (Latimeria) (Coelacanth)
                                                                                                                                                                                                                                                                         55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H(+)(Out).
-!- SUBCELLULAR LOCATION: Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U82228; AAC60322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.4
Best Local Similarity 34.1
Matches 14; Conservative
                                                                                                                                          ; | :| |
73 NYRSLLCC 80
                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                74 EYCNLTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.
                                                                                                                                                                                                                                                                      ATP8_LATCH
O03168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPI1_ECTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                QQ
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                                                                 Db
                                                                                                                QΥ
                                                                                                                                                        연
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I-FUNCTION: NEUROTOXIN, BINDS AND INHIBITS NICOTINIC RECEPTORS.
COMPARED TO ALPRA-NEUROTOXINS, KAPPA-NEUROTOXIN BIND MORE STRONGLY
TO NEURONAL RECEPTORS, AND LESS STRONGLY TO MUSCLE RECEPTORS.
-I-SUBCELLULAR LOCATION: Secreted.
-I-TISSUE SPECIFICITY: Expressed by the venom gland.
-I-SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Venom gland;
MEDLINE=90192091; PubMed=2315018;
Danse J.M., Garnier J.M.;
"cDMA deduced amino-acid sequences of two novel kappa-neurotoxins from Bungarus multicinctus.";
Nucleic Acids Res. 18:1050-1050(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang L.-S., Lin J., Hong E.; "The exon-intron structure of kappa3-bungarotoxin precursor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                         3;
                                                                                                                                                                                                                                                                                                                                                                              Bungarus multicinctus (Many-banded krait).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                   Long neurotoxin CR1 precursor (Kappa neurotoxin) (Kappa3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taiwan banded krait.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                 5 YHGNGQSYRGIFSTIVTGRICQSWSSMIPHRHQRIPENYPNDG 47
                                                                                             LONG NEUROTOXIN CR1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S -> T (IN REF. 2).
A084F400EFE6BB66 CRC64;
                                                                                                                                                                                                                                               P15817; P87353;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 1
Pred. No. 73;
6; Mismatches
                                                                                                                                                                                                                          87 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin; Neurotoxin; Multigene family; Signal,
                       6; Mismatches
  Fred. No. 62;
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X11769; CAA72434.1; -...
PIR; S08398; B60549.
HSSP; P01398; 1KBA.
InterPro; IPR003571; Snake_toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00087; toxin; 1.
ProDom; PD000206; Snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Elapidae; Bungarinae; Bungarus NCBI_raxID=8616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X51413; CAA35775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9660 MW;
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                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
63
79
85
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Matches 20; Conserv
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                bungarotoxin)
                                                                                                                                                                                                                       NXL3_BUNMU
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DISCLEID
DISCLEID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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  Best Local
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                                                                                                                                                                                                     NXL3 BUNNO
                       Matches
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Gaps

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SEQUENCE OF 25-60
   4;
                                        Gaps
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85126393; PubMed-3838275; Prud'Homme J.-F., Eridlansky F., le Cunff M., Atger M., Mercler-Bodart C., Pichon M.-F., Milgrom E.; "Cloning of a gene expressed in human breast cancer and regulated setrogen in MCF-7 cells.";
                                                                                                                                                                                                                             -!- SUBUNIT: Homodimer (Probable).
-!- SIMILARITY: BELONGS TO THE HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence of the pS2 mRNA induced by estrogen in the human breast cancer cell line MCF-7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87146470; PubMed-3822834;
Jeltsch J.-M., Roberts M., Schatz C., Garnier J.M., Brown A.M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -_____ ractor 1 precursor (pS2 protein) (HP1.A) (Breast cancer estrogen-inducible protein) (FNR-2).

HGMO sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 QRTPE----TDPS-IRWEYCRNPDADTGPWCFT----TDPS-IRWEYC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jakowlew S.B., Breathnach R., Jeltsch J.-M., Masiakowski P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 1; Length 72; Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                         ; Iron-sulfur; 4Fe-4S.
34 IRON-SULFUR (4FE-4S) (BY 37 IRON-SULFUR (4FE-4S) (BY 51 IRON-SULFUR (4FE-4S) (BY 65 IRON-SULFUR (4FE-4S) (4FE-4S) (BY 65 IRON-SULFUR (4FE-4S) (4FE-4S) (4FE-4S) (4FE-4S) (4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 12:2861-2878(1984).
                                                                                                                                                                                                                                                                         PIR; S41611; S41611.
HSSP, P38524; 1HPI.
InterPro; IPR000170; Hipot_ironsulf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE~84169578; PubMed=6324130;
                                                                                                                                                                                                                                                                                                                           Pfam; PF01355; HIPIP; 1. PRINTS; PR00374; HIPIPFRDOXIN. PROSITE; PS00596; HIPIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7690 MW;
                                  STRAIN=Beta-1 / DSM 2111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chambon P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFF1_HUMAN
P04155;
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Chambon P. Structure of the human osstrogen-responsive gene p52.", Nucleic Acids Res. 15:1401-1414(1987).

Response Acids Res. 15:1401-1414(1987).

Response Food N.A. Property P. Structure of the human osstrogen-responsive gene P62. Property Prop
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SIMILARITY: Contains 1 P-type (trefoil) domain.
DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/FFFIDD201.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Baloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Gasge by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-96085149; PubMed-8521850; Polshakov V.I., Frenitel T.A., Westley B.R., Chadwick M.P., May F.E.B., Carr M.D., Feeney J.; Keeney J.; MNR-based structural studies of the pNR-2/p52 single domain trefoil peptide. Similarities to porcine spasmolytic peptide and evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Various noxious agents.
Subschild Location: Secreted.
TISSUB SPECIFICITY: FOUND IN STORACH; IS ALSO EXPRESSED IN BREAST CANCER BUT NOT IN NORMAL TISSUE. IT IS REGULATED BY ESTROGEN IN MCF-7 CELLS. STRONG EXPRESSION FOUND IN NORMAL GASTRIC MUCOSA AND IN THE RECENERALIVE TISSUES SURROUNDING ULCEROUS LESIONS OF GASTROINTESTINAL TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gastroenterology 119:691-698(2000).
-1- FUNCIION: Stabilizer of the mucous gel overlying the
gastrointestinal mucosa that provides a physical barrier against
               Mori K., Fujii R., Kida N., Ohta M., Hayashi K.; "Identification of a polypeptide secreted by human breast cancer cells (MCF-7) as the human estrogen-responsive gene (pS2) product."; Blochem. Blophys. Res. Commun. 155:366-372(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS CANCER ILE-32, LYS-32, ASP-34; LYS-37; ILE-46 AND VAL-55. MEDLINE-20440596; PubMed=10983763; Park W.-S., Oh R.-R., Park Y.-Y., Lee J.-H., Shin M.-S., Kim H.-S., Lee H.-K., Kim Y.-S., Kim S.-Y., Lee S.-H., Yoo N.-J., Lee J.-Y.; "Somatic mutations of the trefoil factor family 1 gene in gastric
                                                                                                                                                                                                                    BIOSYNTHESIS, AND SECRETION.
MEDLING-80290699; PubMed-3041593;
Rio M.C., Bellocq J.P., Daniel J.Y., Tomasetto C., Lathe R.,
Chenard M.P., Batzenschlager A., Chambon P.;
"Breast cancer-associated ps2 protein: synthesis and secretion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97250379; PubMed=9096235; MEDLINE=97250379; PubMed=9096235; Polshakov V.I., Williams M.A., Gargaro A.R., Frenkiel T.A., Westley B.R., Chadwick M.P., May F.E.B., Feeney J.; "High-resolution structure of human pNR-2/pS2: a single trefoil motif protein."; J. Mol. Biol. 267:418-432(1997).
                                                                                                                          MEDLINE-89119134; PubMed-3146413; Rio M.-C., Lepage P., Diemunsch P., Roittsch C., Chambon P.; "Primary structure of human protein p52."; C. R. Acad. Sci., III, Sci. Vie 307:825-831(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 233:847-855(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X00474; CAA25155.1; -.
EMBL; X05030; CAA28695.1; -.
EMBL; X05321; CAA28695.1; -.
EMBL; X05322; CAA28695.1; JOINED.
MEDLINE=88326327; PubMed=3261981;
                                                                                                                                                                                                                                                                                                                                 Science 241:705-708(1988).
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AAA52402.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monomeric structure.
                                                                                                                                                                                                                                                                                                                  normal stomach mucosa,
                                                                                                           SEQUENCE OF 25-84.
                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR.
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EMBL;
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14 GTFSTTVTGRICQSWSSMTPHRHQRIPENYPNDGLTMNYCRN----PDADIG-PWCF 65
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D. P25492; P01436;
T. 21-JUL-1986 (Rel. 01, Created)
T. 21-JUL-1986 (Rel. 22, Last sequence update)
T. 28-PEB-2003 (Rel. 41, Last annotation update)
E. Short neurotoxin 1 (Toxin 4).
E. Short neurotoxin 1 (Toxin 4).
S. Enhydrina schistosa (Beaked sea snake) (Common sea snake), and Lapemis hardwickii (Hardwick's sea snake).
C. Ehkaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi; C. Lepidoseuria; squamata; Scleroglossa; Serpentes; Colubroidea;
X. NOBI_TAXID=8682, 8781;
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FEBS Lett. 80:217-220(1977).
-1- FUNCTION: PRODUCES PERIPHERAL PARALYSIS BY BLOCKING NEUROMUSCULAR
TRANSMISSION AT_THE POSTSYNAPTIC SITE. BINDS TO THE NICOTINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-77246775; PubMed-891966; Pox Jh., Blanga M., Tu A.T.; Pox Jw., Blanga M., Tu A.T.; Paring M., Tu A.T.; Parinco acid sequence of a snake neurotoxin from the venom of Lapemis hardwickii and the detection of a sulfhydryl group by laser Raman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Fryklund L., Eaker D., Karlsson E.;
"Amino acid sequences of the two principal neurotoxins of Enhydrina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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EMBL; AB038162; BAB13729.1; -.
EMBL; AP001146; BAA95532.1; -.
EMBL; BC032811; AAH32811.1; -.
PIN: A26667; A26667.
PDB; 1P52; 07-UU-97.
PDB; 1H7; 09-APR-01.
Genew; HGNC1.11759; FFF1.
MIN: 113710; -.
GO; 00:0005975; P: carbohydrate metabolism; TAS.
GO; GO:000511; P: cell growth and/or maintenance; TAS.
InterPro; IPR000519; P-trefoil.
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-!- SIMILARITY: Belongs to the snake toxin family.
PIR; A01705; NIEX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREFOIL FACTOR 1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
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84
71
57
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68
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SEQUENCE OF 1-28 FROM N.A.
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                                                                                                                                                                                                                          5 NQOSSOPKITINCAESSCYKKIWSD---HRGIR-------IERGCGCP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular and cellular analysis of rPl.B in the rat hypothalamus: in situ hybridization and immunohistochemistry of a new P-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                          24; Gaps
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Trefoil factor 3 precursor (Intestinal trefoil factor) (Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Trefoil peptide expression in intestinal adaptation and renewal."; Scand. J. Gastroenterol. Suppl. 192:17-28(1992). [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-80 FROM N.A.
STRAIN=Wistar; TISSUG=Ileum;
MEDLINE-92344598; PubMed=1637322;
Chinery R., Poulson R., Rogers L.A., Jeffery R.E., Longcroft J.M.,
Hanby A.M., Wright N.A.;
"Localization of Intestinal trefoil-factor mRNA in rat stomach and
intestine by hybridization in situ.";
Biochem. J. 285:5-8(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foulsom R., Chinery R., Sarraf C., Lalani E.N., Stamp G., Elia G.,
R InterPro; Irruv...,
JR Pfam; PF00087; toxin; 1.
DR ProDon; PF000205; Snake_toxin; 1.
DR PROSITE; PS00272; SNAKE_roxin; 1.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin; Multigene family.
FT DISULFID 3 22 BY SIMILARITY.
FT DISULFID 41 52 BY SIMILARITY.
FT DISULFID 41 52 BY SIMILARITY.
FT DISULFID 53 58 BY SIMILARITY.
TOTHIFID 53 58 BY SIMILARITY.
TOTHIFID 53 58 TOTHIARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIATE-SQ107881; PubMed=1763017;
MEDIATE-SQ107881; PubMed=1763017;
Sugmenti S., Lynch-Devaney K., Podolsky D.K.;
"Identification and characterization of rat intestinal trefoil factor: tissue- and cell-specific member of the trefoil protein fautor: tissue- and cell-specific member of the trefoil protein fautor: tissue- and cell-specific member of the trefoil protein fautor.
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                                                                                                                                               $; Score 47; DB 1; Length 60;
b; Pred. No. 1e+02;
10; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuropeptide.";
Brain Res. Mol. Brain Res. 33:269-276(1995).
                                                                                                                                                                                                                                                                                                                                           81 AA.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Brain;
MEDLINE-96341837; PubMed-8750886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93068003; PubMed=1439565;
                                                                                                                                                                                                                                                   66 TIDPSIRWEYCNLTRCSD 83
                                                                                                                                                                                                                                                                          43 QVKPGIKLECCHTNECNN 60
                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                 9.0%;
21.8%;
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                                                                                                                                                             Local Similarity 21.89 tes 17; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                               TFF3 OR ITF
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Q03191;
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                                                                                                                                                                                                                STRAIN-Sprague-lawley; TISSUE-Small intestine; STRAIN-Sprague-lawley; TISSUE-Small intestine; MEDLINE-97445097; PubMed-9299425; Tan X.D., Hsueh W., Chang H., Wei K.R., Gonzalez-Crussi F.; Tan X.D., Tauterization of a quatrier receptor for intestinal trefoil factor in rat small intestine: identification by in situ binding and ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 FWTTLLIVLVAGSSCKAQEFVGLSPSQCMVPANVRVDCGYPT--VTSGQCNNRGCCFDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 FSTT-----VTGRTC--QSWSSMTPHR-----HQRTPENYPNDGLTMNYCRN-----
                                                                                                                                                                                                                                                                                                                                              Sands B.E., Ogata H., Lynch-Devaney K., Debeaumont M.,
Ezzell R.M., Podolsky D.K.;
"Molecular cloning of the rat intestinal trefoil factor gene.
Characterization of an intestinal goblet cell-associated promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.8e+02;
8; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
T -> I (IN REF. 2 AND 5).
V -> A (IN REF. 1).
G -> N (IN REF. 1).
G -> N (IN REF. 1).
915052312C7B517E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 P-type (trefoil) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
TREFOIL FACTOR 3.
                                                                                                                                                 J. Biol. Chem. 270:9353-9361(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, 766956, 7AC52439.1; -.
EMBL, 766956, 0AA47378.1; -.
EMBL, 549317; AAB24079.2; ALT_SEQ.
EMBL, U20984; AAB01063.1; -.
                       MEDLINE=95238450; PubMed=7721858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000519; P_trefoil. Pfam; PF00088; trefoil; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00025; P_TREFOIL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M80826; AAA42270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U20984; AAB01063.1; -.
EMBL; AF012534; AAB71352.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8944 MW;
                                                                                                                                                                                                SEQUENCE OF 22-81 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTREFOIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTESTINAL EPITHELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 -PDADTGPWCF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 IPNV---PWCF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
81
73
70
70
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A41441; A41441.
PIR; A56366; A56366.
PIR; UC5623; PIR; S23963; A23963; A523963; A523963.
STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00018; PD;
PROSITE; PS00025; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 19: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA;
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SCIT_MESTA

RESULT 11

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                            Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Openhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi; Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                             Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA-THIONIN HOMOLOG AT2G02100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45.5; DB 1; Length 77; Pred. No. 1,9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. C24, TISSUB=Flower buds;
Mache R., Quigley F., Thomas F., Yu D.Y.;
Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GTFSTTVTGRICQSWSSMTPHRHQRTPENYPNDGLIMNYCRN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GMGPVTVEARICESOS----HRFKGTCVSASN---CANVCHN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
ECO4E660C3610965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELIUIAR LOCATION: Secreted (Potential).
-!- SIMILARITY: BELONGS TO THE PLANT DEFENSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 6.0 kDa protein in COSI 5'region.
YNE338W OR NO170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.9e+
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 228455; CAA79189.1; -...
PIR, S30578; S30578.
HSSP, P2020.1 GPT.
INTERPRO; IPR003218; Gamma-thionin.
InterPro; IPR003614; Knotl.
Probom; P200354; Gamma-thionin; 1.
PROSITE; P80094; GaMma-THIONIN; 1.
PROSITE; P80094; GAMMA_THIONIN; 1.
Plant defense; Signal; Multigene family.
SIGNAL
CHAIN
DISULEID
DISULEID
17 GAMMA_THIONIN I
DISULEID
17 BY SIMILARITY.
DISULEID
50 71 BY SIMILARITY.
DISULEID
51 77 BY SIMILARITY.
DISULEID
52 77 AA; 8524 MW; EC04E660C361096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Obermaier B., Piravandi E., Rinke M.;
MEDLINE=20083487; PubMed=10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X69139; CAA*0022...,
EMBL; AC005936; AAC97223.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X69139; CAA48892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%;
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Best Local Similarity 35.000
Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-75 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YN78_YEAST
P53820;
                                                                                                                                                                                                                                                                                                                                                       thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YN78_YEAST
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   δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOTALION TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-ocr-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
38-FBB-20010 OR F504.13.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                       Lepidopteran-selective toxin (ButaIT).
Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wudayagiri R., Inceoglu B., Herrmann R., Derbel M., Choudary P.V.,
Hammock B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of a novel lepidopteran-selective toxin from the venom of South Indian red scorpion, Mesobuthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-cv. C24; TISSUE-Flower buds; Yu D.Y., Quigley F., Mache R.; "Isolation and expression of a cDNA encoding protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45.5; DB 1; Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
FD36529E5FA7CCD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 AA.
                                                                 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 87;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPWCFTTDPSIRWEYCNLTRCSDTEG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THG1_ARAIH STANDARD; P 039182; 042011; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence-2003 (Rel. 41, Last anno-28-FEB-2003 (Rel. 41, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
27
32
34
3864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMC Biochem. 2:16-16(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
PubMed=11782289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECTROMETRY
                                                                                                                                     28-FEB-2003
                                                                                                                                                                      28-FEB-2003
                                                                                                                                                                                                          28-FEB-2003
                                                                    SCIT_MESTA
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Best Local
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5

Gaps

RESULT 12 THG1_ARATH

Matches

Qγ В

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Hydrophis lapemoides
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                       59 AA;
                                                                                                 117
43
118
118
118
118
130
130
                                                                                                DISULFID
DISULFID
DISULFID
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  셤
                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no with modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing glycoprotein IIb-IIIa (alpha IIb-beta 3) antagonist with a neurotoxin fold.";
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 226:861-868(1994).
-!- FUNDTION: INHIBITS ADP-INDUCED PLATELET AGGREGATION AND INHIBITS
THE BINDING OF PURIFIED PLATELET FIBRINGEN RECEPTOR GPILB-ILIA
TO IMMOBILIZED FIBRINGGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95112851; PubMed=7813476; Jaseja M., Lu X., Williams J.A., Sutcliffe M.J., Kakkar V.V., Parslow R.A., Hyde E.I.; Pud Secondary structure of dendroaspin, an RGD-"IH-NMR assignments and secondary structure of dendroaspin, an RGD-"
                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
48-ADB-2003 (Rel. 41) Last annotation update)
48-EDB-2003 (Rel. 41) Last annotation update)
58-FEB-2003 (Rel. 41) Least annotations (Platelet aggregation inhibitor) (Dendroaspia)
58-FEB-2003 (Rel. 41) Relaced (Eastern Jameson's mamba).
58-FEB-2003 (Rodadas (Caniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDowell R.S., Dennis M.S., Louie A., Shuster M., Mulkerrin M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazarus R.A.; "Mambin, a potent glycoprotein IIb-IIIa antagonist and platelet aggregation inhibitor structurally related to the short
                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-95360732; PubMed=7634091;
Sutcliffe M.J., Jaseja M., Hyde E.I., Lu X., Williams J.A.;
"Three-dimensional structure of the RGD-containing neurotoxin
                                                                                                                                                                                                                                                                            23 RTCQSWSSM-----TPHRHQRTPENYPNDGLTMNYCRNPD 57
                                                                                                                                                                                                                                                                                            4 RPCLTPSSMQYSDIYIPTPTPTPTPTPTPTPTHTHTHTHNPN 48
                                                                                                                                                                                                                          Score 45; DB 1; Length 52; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                    17; Indels
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Expressed by the venom gland.
                                                                                                                                                                                                  C1E4066D43E057A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 59 AA.
                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom;
MEDLINE=92273586; PubMed=1591238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elapidae; Elapinae; Dendroaspis.
NCBI_TaxID=8619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 31:4766-4772(1992).
                                                                                                                                            EMBL; 271613; CA96273.1; -. PIR; S63324; S63324. S605282; YNL338W.
                                                                                                                                    EMBL; Z71614; CAA96274.1; -.
                                                                                                                                                                                                                           8.6%;
                                                                                                                                                                                      al protein.
52 AA; 5951 MW;
                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maeda N., Tamiya N.;
"Three neurotoxins from the venom of a sea snake Astrotia stokesii,
including two long-chain neurotoxic proteins with amidated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mori N., Tu A.T.; In A.T.; It is a structure of the major toxin from sea snake, "Isolation and primary structure of the major toxin from sea snake,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Hydrophilnae; Astrotia.
                                                                                                                                                                                                                                                                                                                               CELL ATTACHMENT SITE (POTENTIAL).
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P01438; P10461; P19005;
21-071-1986 (Rel. 01, Created)
23-1071-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Short neurotoxin 1 (Toxin A).
Astrotia stokesi (Stokes's sea snake) (Disteira stokesi),
Hydrophis ornatus (Reef sea snake), and
Acalyptophis peronii (Sea snake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 59;
Pred. No. 1.6e+02;
8; Mismatches 28; Indels
PDB; IDRS; 20-DEC-94.
InterPro; IPR003571; Snake_toxin.
Fran; PF00087; Loxin; 1.
ProDom; PD000206; Snake_toxin; 1.
PROSITE; PS00722; SNakE_TOXIN; FALSE_NEG.
DISULED Coagulation; Cell adhesion; Toxin; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6754 MW; 20DDC6A5D9DF9E41 CRC64;
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MEDLINE-83308533; PubMed-6615431;
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SPECIES=A.peronii; TISSUE=Venom;
MEDLINE-88132805; PubMed=3341735;
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RM (4)

RM Arch. Biochem. Biophys. 260:10-17(1988).

RM (5)

RESCRIESA. PECTOMI; TISSUE-Wenom;

RA MEDILINE-89176487, PubMed=3202959;

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RM MEDILINE-89176487, PubMed=3202959;

RM MEDILINE RECENTANT STEEN PROFINITY RECENTION RUNG/MED THE MINORITY CONTRICT CON
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Search completed: September 29, 2003, 08:34:03 Job time: 24 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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	RESULT 1	ID Q9UMI2 PRELIMINARY; PRT; 53 AA.	Q9UMI2;	01-MAY-2000 (TrEMBLrel, 13,	DT 01-MAY-2000 (TremBirel. 13, Last sequence update)	PIG protein (Fragment).	PLG.	Eukaryota; Metazoa; Chordata;	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX NCBI_TaxID=9606;	RN [1]	RP SEQUENCE FROM N.A.	RX MEDLINE=85023311; PubMed=6148961;		RT human and bovine plasminogen.";	RL Biochemistry 23:4243-4250(1984).	CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN,	DR EMBL; K02921; AAA60123.1;	DR HSSP; P00747; 2PK4.	DR InterPro; IPR000001; Kringle.	DR Pfam; PF00051; kringle; 1.	DR PRINTS; PR00018; KRINGLE.	DR ProDom; PD000395; Kringle; 1.	DR SMART; SM00130; KR; 1.	DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.	DR PROSITE; PS50070; KRINGLE_2; 1.	KW Glycoprotein; Kringle.	FT NON TER 1 1	SQ SEQUENCE 53 AA; 5893 MW; 2EB36E715CD40A47 CRC64;	Similarity 82.2%; Pred. No. 1.1e-18;	Matches 37; Conservative 4; Mismatches 4; Indels
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1 VRQCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPN 45

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2928 MW; BEEDD4C62FA480A8 CRC64;

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25 AA;
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 SEQUENCE
                             Query Match
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Matches
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                                                                                                                                                             RESULT 4
                                                                                                                                                                          Q9BGN9
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X MEDLINE-21181705; PubMed=11285247;
A Ogocalkova M., Kraft H.G., Ebhholm C., Utermann G.;
A Ogocalkova M., Kraft H.G., Ebhholm C., Utermann G.;
Types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucastans.";
I types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucastans.";
I thum Anno. Genet. 10:815-824(2001).
C. -: SIMILARITY: CONTAINS I KRINGLE DOMAIN.
R HSSP; PO0747; IKRN.
RR HSSP; PO0747; IKRN.
RR Pfam; PF000031; Kringle: 1.
R PRODOR; PR000039; Kringle: 1.
R PROSITE; PS000031; KRINGLE_1; 1.
R PROSITE; PS00013; KRINGLE_1; 1.
R PROSITE; PS00013; KRINGLE_1; 1.
R PROSITE; PS00013; KRINGLE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94060120; PubMed=7848387;
Pfaffinger D., Mc Lean J., Scanu A.M.;
"Amplification of human APO(a) kringle 4-37 from blood lymphocyte
DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
APO(A) KRINGLE 4-37, APO(A) KRINGLE type 5 (Fragment).
HOMO Sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Frimètes; Catarrhini; Moninidae; Homo.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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1 GLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCLVTESSVL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 GLTMNYCRNPDADTGPWCFTTDPSIRWEYCNLTRCSDTEGTVV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 60
60 AA; 6799 MW; 5719AA26B3E0FFID CRC64;
                                                                                                               01-MAY-2000 (TrENBLrel. 13, Created)
01-MAY-2000 (TrENBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AA.
                                                                                        60 AA
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HSSP, P00747, TKRN.
InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Kringle; Lipoprotein.
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                                                                                                                                                               Apolipoprotein(a) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                        PRELIMINARY;
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                                                                                                                                                                                         Homo sapiens (Human).
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                                                                                                      090KJ7
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                                                          RESULT 2
Q9UKJ7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CD_331V3;
Machado D.M., Delwart E.L., Diaz R.S., Oliveira C.F., Rawal B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Uterus;
Murakami S., Fujiwara C., Miyamoto Y., Takeuchi S., Takahashi S.,
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Score 141; DB 4; Length 25; Pred. No. 1.6e-09; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBirel. 17, Created)
01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-MR-2003 (TrEMBIrel. 23, Last annotation update)
Hepatocyte growth factor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watch 24.4%; Score 127.5; DB 6;
Local Similarity 52.8%; Pred. No. 2.1e-07;
nes 19; Conservative 9; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 NYCRNPDADT-GPWCFTTDPSIRWEYCNLTRCSDTE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NYCRNPRGEEGGPWCFISNPEVRYEVCDIPQCSEVE 36
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                                                                                                                                                                                                                                           75 AA
                                                                                         64 CFTTDPSIRWEYCNLTRCSDTEGTV 88
                                                                                                               1 CFTMDPSIRWEYCNLTRCSDTEGTV 25
                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 2.
SWART; SW00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8831 MW;
    ch 27.0%;
1 Similarity 96.0%;
24; Conservative
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                          Best Local Similarity
Matches 24; Conserv
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SEQUENCE FROM N.A.
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Gaps

9;

87;

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10 WGSPLPEILGGARSRYQLITEGPSADPGLENSKIRVNSCHR------WCFKREISIR-D 61
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                                                                                                                                                                                                                                                                                                                               35 RHQRIPEN-YPNDGLTMNYCRNPDADIGPWCFITDPSIRWEYCNLT---RCSDTEGIVV 89
                                                                                                                                                                                                                                                                                                                                                                 12 RHOAWPATAMEDDGRKDDAAAAPGRDSHRW-----POIRWRPCORPPRHCSTPPGRAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usuda Y., Sugimoto S.,
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP065219; BAC18299.1; -
Hypotherical protein; Complete protecome.
SEQUENCE 85 AA; 9868 MW; AA74412387441A4A CRC64;
Oryza sativa (japonica cultivar-group).
Bukaryoca: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzaee; Oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y., Ikeo K., Suzuki M., Mashima J., Itch T., Yamagishi A., Nishio Y.,
                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium. NCBL_TaxID-152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%; Score 53.5; DB 16; Length 85; 27.0%; Pred. No. 97; ive 6; Mismatches 19; Indels 2:
                                                                                                                                                                                                                                                            Score 55.5; DB 10; Length
Pred. No. 58;
3; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                             10.6%;
30.5%;
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Best Local Similarity 27.05
Matches 17; Conservative
                                                                                                                                                                                                                                                                              18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. CE1489.
                                                                                        [1]
SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=39947;
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Best Local Si
Matches 18;
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   4;
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                                                                                                                                                                                                                                                                                              41 ENYPNDGLTM------NYCRNPDADT------GPWCFTTD--PSIRWEYCN--LT 79
                                                                                                                                                                                                                                                                                                                    Toossi Z., Arts E.;
"A TB-mediated Site Specific Increase in HIV-1 Quasispecies Diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins K., Quinones-Mateu M., Wu M., Luze H., Johnson J., Hirsch C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May Lead to the Observed Greater HIV-1 Heterogeneity in Patients Co-
infected with Tuberculosis.",
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF383521;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                "Use of the Dual Sensitive/Less-Sensitive (Detuned) EIA Strategy for Targeting Genetic Analysis of HIV-1 to Recently Infected U.S. Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 NDGLTMNYCRNPDADT----GP---WCFTTD--PSIRWEYCNLTRCSDTE 85
                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                             DB 15; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56; DB 15; Length 87; Pred. No. 51; 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                             18; Indels
                                                                 Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AE373767; AAK55387.1; -.
InterPro; 1PR070777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                        9895 MW; 1A0C197C8C58A808 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Envelope 91ycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID-11676;
Sullivan M., Gwinn M., Clark K.A., Busch M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 AA.
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                                                                                                                                                                                                                           11.4%; Score 59.5; D
30.0%; Pred. No. 20;
tive 10; Mismatches
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01-WAR-2003 (TrEMBLrel. 23, Last sequ
01-WAR-2003 (TrEMBLrel. 23, Last anno
0407H12.22 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                      AIDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.7%;
Best Local Similarity 32.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                             Local Similarity 30.09 nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 80 RCSDIEGIVV 89
                                                                                                                                                                                                                                                                                                                                                                                                  KWNDTLKQIV 79
                                                                                                                                                                                          86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AA;
                                                                                                                                                                        98
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SEQUENCE
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SEQUENCE
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Q8H444;
                                                                                                                                                        NON_TER
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                                                      Donors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q90BU2
                                                                                                                                                                                                                                                             Matches
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RESULT 6

δ g ŏ g Q90BU2

Gaps

21;

RESULT 7

δŽ 셤 Q8H444

SEATAGE

'n

Gaps

11;

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45 NDGLTMNYCRNPDADT -----GPWCFTTD -- PSIRWEYCNL -- TRCSDTEGTVV
                                                                                                                     MEDLINE-9938830; PubMed-10461834; MEDLINE-99388930; PubMed-10461834; Mavas M.C., Letourneur E., Gomas E., Boshell J., Saragosti S.; "Analysis of the V3 loop sequences from 12 HIV type-1 infected patients from Colombia, South America."; AIDS Res. Hum. Retroviruses 15:1141-1144(1999). EMEL; Y10364; CAA71393.1; -. Fams. PRO0516; CA2077; GP120. Pfam; PRO0516; CP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navas M.C., Letourneur E., Gomas E., Boshell J., Saragosti S.;
"Analysis of the V3 loop sequences from 12 HIV type-1 infected
patients from Colombia, South America.";
AIDS Res. Hum. Retroviruses 15:1141-1144(1999).
BEMBL; Y10366; CRA7195.1;
Interpro; IPR00777; GF120.
Pfam; PF00516, GF120; 1.
MIDS; CCat protein, Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.5; DB 15; Length 88;
Pred. No. 1.3e+02;
8; Mismatches 12; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.0%; Score 52.5; DB 15; Length 89; illarity 31.6%; Pred. No. 1.3e+02; Conservative 10; Mismatches 16; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 NDGLTMNYCRNPDADT-----GPWCFTTD--PSIRWEYCNLTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 AA; 9884 MW; 88ADA051D4AD1E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 AA; 9858 MW; 688C7D9A96FFE10F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TIEMBLRel. 15, Created)
01-0CT-2000 (TIEMBLRel. 15, Last sequence update)
01-0CT-2002 (TIEMBLRel. 22, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Tissue plasminogen activator (Fragment).
Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=COL694;
MEDLINE-99388930; PubMed-10461834;
                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%;
32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
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les 18; Conserv
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                                                                            SEQUENCE FROM N.A. STRAIN=COL692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9MZE7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9MZF7
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STRAIN-SA98V153.

WEDLINE-21405813; PubMed=11514720;
Venter M., Madhi S.A., Tiemessen C.T., Schoub B.D.;
Venter M., Madhi S.A., Tiemessen C.T., Schoub B.D.;

"Genetic diversity and molecular epidemiology of respiratory syncytial virus over four consecutive seasons in South Africa: identification of virus over four consecutive seasons in South Africa: identification of virus over four and B genotypes.";

J. Gen. Virol. 82:217-2144(2001).

EMBL; AF848815; AAL60316.1;

TINCEPPO; IPRO00925; Glycoprot.G.

Pfam; PF00802; Glycoprotein.G; 1.
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                                                                                                                        Naghavi M.H., Salminen M.O., Sonnerborg A., Vahlne A.;
"DNA sequence of the long terminal repeat of human immunodeficiency
virus type 1 subtype A through G.";
AIDS Res. Hum. Retroviruses 15.485-488(1999).
EXMED, AFT06123, AAD16901.1;
InterPro; IPR000777; GP120.
Pfan; PF00516, GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.0%; Score 52.5; DB 12; Length 87; Best Local Similarity 34.9%; Pred. No. 1.3e+02; Matches 15; Conservative 1; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 NDGLTMNYCRNPDADT-----GPWCFTTD--PSIRWEYCNLTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 GNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 GTSTSQSTVLDTTTSKHTIQQQS----LHSTTPENTPNSTQT 68
                                                                                                                                                                                                                                                                                                                                                          82 AA; 9408 MW; 731C8B5B2D075638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AA; 9431 MW; CEF8B4DD27344769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8V513;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Attachment glycoprotein G (Fragment).
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01-0CT-2000 (TIEMBLIAL. 15, Last sequence update)
01-0CT-2002 (TIEMBLIAL. 22, Last annotation update)
ENVELOPE PROCEIN (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                      Score 52.5; DB 15
Pred. No. 1.2e+02;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                            STRAIN-UG5609;
MEDLINE-99210134; PubMed-10195759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus.
                                                                                                                                                                                                                                                                                       Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                        10.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Matches 16; Conserv
                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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       NCBI_TaxID=11676;
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SEQUENCE
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Q9ID04;
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Search completed: September 29, 2003, 08:35:46 Job time: 97 secs
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Gallus gallus (Chicken).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia! Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
                                                                                                                                               MEDLINE=20380829; PubMed=10920240; Scotegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L., Sonstegard T.S., Garrett W.M., Ashwell M.S., Bennett G.L., Kappes S.M., Van Tassell C.P.; "Comparative map alignment of BTA27 and HSA4 and 8 to identify conserved segments of genome containing fat deposition QTL."; Mamm. Genome 11:682-688(2000).
EMBL; AF230195; AAF79125.1; "HSSP; P00705, 1TPG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%; Score 52; DB 6; Length 39;
50.0%; Pred. No. 61;
Ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamajima S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AA; 4296 MW; BDB3A28B38A67ECB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Riboflavin binding protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-88298752; PubMed=3403518; Zheng D.B., Lim H.M., Pene J.J., White H.B.; "Chicken riboflavin-binding profesin."; J. Biol. Chem. 263:11126-11129(1988). EMBL; AB022344; BAA37125.1; -. InterPro; IRR04269; Folate_rec. Pfam. PF03024; Folate_rec. 1.
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                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR006209; EGF_like.
InterPro: IPR00001; Kringle.
Prosite: Prosite: Kringle: 1.
PROSITE: PR00128; EGF_1: 1.
PROSITE: PS01188; EGF_2: 1.
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28.2%;
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Best Local Similarity 28.2
Matches 11; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Kringle.
NON_TER 1 1
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46
46 AA;
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NON_TER
SEQUENCE
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Gaps
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MEDLINE-20170311; Pubmed-10708058;
MEDLINE-20170311; Pubmed-10708058;
Gasado C., Urtasun I., Martin-Walther M.V., García S., Rodriguez C.,
del Romero J., Lopez-Gallindez C.;
"Genetic analysis of HIV-1 samples from Spain.";
J. Acquir. Immune Defic. Syndr. 23:68-74(2000).
EMBL: AF152790; AAF08428.1;
InterPro; IPR000777; GP120.
AIRS: RO0316; GP120;
AIRS: Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.9%; Score 52; DB 15; Length 67; Best Local Similarity 32.7%; Pred. No. 1.1e+02; Matches 16; Conservative 8; Mismatches 13; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 CRNPDADT-----GPWCFTTD--PSIRWEYCNLTRC--SDTEGTVV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AA; 7564 MW; 7969874F7D8BBD6E CRC64;
15 TFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYC 53
                                               7 TLFAVITSSTCQQYGCLEGDTHKANPSPEPN----MHEC 41
                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLRel. 13, Created)
01-MAY-2000 (TrEMBLRel. 13, Last sequence update)
01-OCT-2002 (TrEMBLRel. 22, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID-11676;
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                                                                                                                                                                                                    PRT;
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SEQUENCE
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September 29, 2003, 08:36:39; Search time 82 Seconds (without alignments) 166.469 Million cell updates/sec
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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1 EQDCMFGNGKGYRGKKATTV......YTWNPRKLFDYCDIPLCASS 86
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                       - protein search,
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score 1 508 2 413 3 424.5 5 258.5 6 258.5	% Match Match 100.0 81.3 81.3 54.0 50.9 50.9	% watch Length DB Match Length DB 86 22 81.3 79.7 79 18 54.0 79 17 50.9 82 21 50.9 84 10	DB 22 22 17 17 17 17 17 17 17 17 17 17 17 17 17	ID AAY 2947 AAB 08413 AAW 1926 AAW 07546 AAW 07548 AAY 7719 AAP 93230	Description Human apolipoprote Amino acid sequenc Human plasminogen Khesus kringle 1. Bovine kringle 1. Human plasminogen Plasminogen kringl
6 258.5	200	84	77	AABULYUS	Human plasminogen
9 256.5	50.5	79	17	AAW07545	human kringle 1

WPI; 2001-244787/25. N-PSDB; AAD03258.

	01	254	٥.	81	10		Synthetic N-termin
_	_	52	6	84	21	-	Amino acid sequenc
	7	51	9.	79	φ	AAP81360	K1 domain of plasm
~	(3	51	6	79	17	AAR96221	
	14	48	ω,	78	10	AAP94401	Sequence encoding
	5	246.5		79	17	AAW07547	~
	9	47	7	79	17	AAW07544	murine kringle 1.
	17	2	7	78	17	AAW07559	Murine kringle 4.
П	8	238.5	ė.	86	23	ABP02801	Human ORFX protein
<u>, , , , , , , , , , , , , , , , , , , </u>	61	2	è	82	10	AAP93231	Plasminogen kringl
. 1	20	235	46.3	84	21	AAY7720	Human plasminogen
(1	27	223	e,	82	21	AAB01907	Human plasminogen
. 1	22	222	æ,	78	17	AAW07554	Murine kringle 3.
. 1	33	222	ω.	78	17	AAW07560	Human kringle 4.
. 1	34	220	ω,	78	17	AAW07553	Bovine kringle 2.
. 4	35	220	ω,	78	17	AAW07557	
	36	217	ζ.	78	17	AAW07549	Murine kringle 2.
	37	217		83	21	AAB01908	plasmino
	38	216		78	17	AAW07550	kringle 2
. 1	39	216	ď	78	17	AAW07551	Rhesus kringle 2.
,	30	215	•	78	17	AAW07555	Human kringle 3.
1.1	31	215	•	78	17	AAW07552	kringle
,	32	215	•	78	17	AAW07556	Rhesus kringle 3.
4-1	33	213	•	78	17	AAW07558	Bovine kringle 3.
4-7	34	213	•	78	21	AAY77721	Human plasminogen
•••	35	213		83	21	AAB08414	Amino acid sequenc
4.)	36	212	ij	83	21	AAB08412	acid
4-)	37	194	ω ω	82	21	AAB08411	acid
,	38	149	•	47	13	AAR25682	
1-7	39	146	ω.	32	23		Plasminogen peptid
7	10	136	ė,	30	23	AAU98483	Plasminogen peptid
7	17	135	ė.	38	21		Human plasminogen
7	17	31	ς.	44	13	AAR25688	Exon XI of human h
7	13	30	'n	72	22		Human kringle doma
7	‡ 4	128.5	'n.	42	22	ABG48942	Human liver peptid
7	12	28	'n	42	22	94	
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RESULT	T !						

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Human, angiogenesis inhibitor; LK8; apolipoprotein(a) kringle domain; angiogenesis-mediated disease; cancer; rheumatoid arthritis; therapy; cytostatic, antirheumatic; antiarthritic; antipsoriatic; psoriasis; ocular angiogenic disease; endothelial cell proliferation; tumour; cell migration.
                                                                             Human apolipoprotein(a) kringle domain V38, LK8 protein.
                                                                                                                                                                                                                                                                                                              Chung S;
                                                                                                                                                                                                                                                                                      (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                            Yum J,
             AAY72947 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                            Chang J, Kim JS, Park EJ,
                                                                                                                                                                                                                                          99WO-KR00554
                                                                                                                                                                                                                                                                99WO-KR00554
                                                         (first entry)
                                                                                                                                                                                            WO200119868-A1.
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                        15-SEP-1999;
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                                                        13-JUN-2001
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AAY72947
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AAW19256
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                                                                                                                                                                                                                                                                                                                   The present sequence is human LK8 protein which contains the amino acid sequence of human apolipoprotein(a) kringle domain V38 (KV38). The human apolipoprotein(a) kringle domains LY36 (LK6 protein), IV37 (KW protein) and V38 (LK6 protein) together form the angiogenesis inhibitor. LK68 protein. LK68, LK6, LK7 and LK8 are inhibitors are of endothelial cell proliferation, cell migration and normal development of capillaries in the chick embryo choricallantoin membrane (CAM). LK68 protein, its single kringles or their functional equivalents, are useful for treating angiogenesis-mediated diseases, such as cancer, rheumatoid arthritis, psoriasis or ocular angiogenic also for inhibiting primary tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitor; KED; kringle protein, angiogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distrass syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
        Novel angiogenesis inhibitor, LK68 for treating angiogenesis-mediated diseases, e.g. cancer and rheumatoid arthritis, has human apolipoprotein(a) kringle domains IV36, IV37 and V38 amino acid
                                                                                                                                                                                                                                                                                                        1 EQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGD
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
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0
                                                                                                                                                                                                                                                            DB 22; Length 86;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of kringle 5 of human plasminogen.
                                                                                                                                                                                                                                                   Score 508; DB 22;
Pred. No. 1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dou D, Chopp M, Wang L, Mikkelsen T;
                                                                                                                                                                                                                                                                                                                                                               61 INGPWCYTMNPRKLEDYCDIPLCASS 86
                                                                                                                                                                                                                                                                                                                                                  61 INGPWCYTMNPRKLFDYCDIPLCASS 86
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08413 standard; Protein; 85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FORD-) FORD HEALTH SYSTEM HENRY.
                                                                 Claim 3; Page 47; 50pp; English.
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99US-0121633.
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                                                                                                                                                                                                                                                                                 86; Conservative
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                                                                                                                                                                                                                                                                     Local Similarity
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                                                  The specification describes a human polypeptide which is a potent angiogenesis inhibitor, and is designated KED. KED polypeptide, Kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome, castleman's disease, psoriasis, hepatilis, aneurysm, renal disease and haemangioma. The present sequence represents kringle 5 of human plasminogen, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BEDCMFGNGKGYRGKRATTVTGTPCQQWAAQEPHRHSTFTPETNPRAGLEKNYCRNPPQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasminogen; Kringle 5; cell proliferation inhibitor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 413; DB 21;
Pred. No. 2.3e-33;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 INGPWCYTMNPRKLFDYCDIPLCAS 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : |||||| | |||:||||:| ||:
61 VGGPWCYTTNDRKLYDYCDVPQCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
Disclosure; Fig 6; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.3%;
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95US-0008519.
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Best Local Similarity 80.0°
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13-DEC-1995;
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79 AA;
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Best Local S:
Matches 47;
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                                                                                                                                                                                                            1 CMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibiting endothelial cell proliferation, using as active component an anglostatin fragment, a combination of anglostatin fragments, or aggregate anglostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BKLS protein. The aggregate anglostatin has a Mol. Wto 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating anglogenesis-mediated diseases such as cancer, arthritis, macular
                                                             wound
         corneal diseases, rubeosis, neovascular glaucoma, diabetic retinogathy, retrolental fibroplasia, arthritis, diabetic neovascularisation, muscular degeneration, peptic ulcer, Helicobacter related disease, fractures, keloids, vasculogenesis, hematopoiesis, ovulation, menstruation, placentation or cat scratch fever, and to stimulate wound healing. The protein and antibodies generated from it can be used to green for agonists and antagonists or in detection, imaging and
                                                                                                                                                                                               4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
                                                                                                                                                                         Gaps
collaterals, arteriovenous malformations, ischemic limb angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                   angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                        ;
0
                                                                                                                                                Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new methods and compositions for
                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim KL;
                                                                                                                                              Score 405; DB 18;
Pred. No. 1.3e-32;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Folkman MJ, Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Pages 104-105; 203pp; English.
                                                                                                                                                                                                                                                                                                                                   AAW07546 standard; protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                               64 PWCYTMNPRKLFDYCDIP 81
                                                                                                                                                                                                                                                             |||||| ||||||:||||:|
PWCYTTNPRKLYDYCDVP 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0429743.
96US-0605598.
                                                                                                                                              79.7%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US05856.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                        66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-518662/51
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus kringle 1.
                                                                                                                       79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1995;
22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-1996
                                                                                                 diagnosis.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                          AAW07546;
                                                                                                                                               Query Match
Best Local S
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The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragment, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 1, kringle 1-3, kringle 1-3, kringle 1-3, kringle 1-4, kringle 1-3, kringl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKTGNGKNYRGTMSKTRTGITCQKWSSTSPHR-PTFSPATHPSEGLEENYCRNPDNDGQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
degeneration and diabetic retinopathy. It can also be used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis; cancer; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                            antibodies for use in diagnosis, detection and therapy. The present sequence, Rhosus Kringle 1, is a specific angiostatin fragment which can be used in the invention, and represents amino acids 6-84 of Rhesus angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 274.5; DB 17;
Pred. No. 9.4e-20;
8; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sim KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiostatin; plasminogen; kringle; angloger
macular degeneration; diabetic retinopathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 106; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW07548 standard; protein; 79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PWCYTTDPEBREDYCDIPEC
                                                                                                                                                                                                                                                                                                                                                                                                                              54.0%;
58.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.8 tes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-518662/51.
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(angiostatin).
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03-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8910401-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                           AAP93230;
                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                            scu-PA;
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ID AAPS
                                                                                                                                                                                                                                                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides fragments of kringle 1, 2 or 4 of human plasminogen that contain a lysine binding site and have anti-angiogenic activity. The peptides of the invention function as antiangiogenic activity. The peptides of the invention function as antiangiogenic agents, for the treatment process and diseases involving angiogenesis. Such diseases include cancers such as solid tumours, blood born tumours such as leukemias, tumours metastasis, benign tumours such as hemangiomas, acoustic acurcomas, neurofibromas, trachomas and pyogenic granulomas, rheumatoid arthritis, ocular angiogenic diseases such as diabetic retinopathy, retinopathy of prematurity, mecular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber syndrome, myocardial angiogenesis, plaque corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, and wound granulation, The fragments are also useful in treatment of disease of excessive or abnormal stimulation of endothelial cells. These
                                                                         7
                                                                                                                                                                                                                                                                                                                                 Kringle 1; plasminogen; anti-angiogenic; angiogenesis; angiostatin; cytostatic; antiarthritic; antisheumatic; antidabetic; ophthalmological; immunosuppressant; vasotropic; vulnearay; antiarteriosclerotic; human; dermatological; cancer; tumour; birth control; vascularization.
                                                                                                 63
                                                                                                            4 CMFGNGKGYRGKKATIVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel lysine binding fragments angiostatin used as antiangiogenic agents in the treatment of cancer, diabetic retinopathy, rheumatoid arthritis, psoriasis, atherosclerotic plaque formation, and other angiogenesis diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                36..73
/note= "specifically claimed fragment (AAX77722)"
                                                                         1;
                                                 DB 17; Length 79;
                                                                         Indels
                                             Score 258.5; DB 1
Pred. No. 3.5e-18;
7; Mismatches 26
                                                                                                                                                                                                                                                                                                         Human plasminogen kringle 1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                   AAY77719 standard; protein; 82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 30pp; English.
acids 6-84 of bovine angiostatin.
                                                                                                                                                83
                                                                                                                                                                      PWCYTTDPDKRYDYCDIPEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBE CO.
                                                                                                                                                PWCYTMNPRKLFDYCDIPLC
                                              50.9%;
nilarity 57.5%;
Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US15271.
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                                                                                                                                                                                                                                                                                   (first entry)
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                                                           Local Similarity
es 46; Conserv
                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ji R, Trail PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200003726-A1.
                         4
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                  12-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2000
                                                                                                                                                64
                                                                                                                                                                                                                                                            AAY77719;
                           Sequence
                                               Query Match
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Region
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diseases include intestinal adhesions, atherosclerosis, scleroderma, and hypertrophic scars. The fragments can be used as birth control agents by preventing vascularization required for embryo transplantation. The present sequence represents the kringle 1 sequence of human plasminogen
                                                                                                                                                                                                                                                                                                      3 DCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDIN
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                    82;
                                                                                                                                                                                                 Score 258.5; DB 21; Length Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified plasminogen activator - having greater fibrin selectivity and circulating halflife.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasminogen; activator; t-PA; fibrin; kringle domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasminogen kringle 1 domain (residues 79-162).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                    9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP93230 standard; peptide; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; fig 3A; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        63 GPWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GPWCYTTDPEKRYDYCDILEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLB ) COLLABORATIVE RES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
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                                                                                                                                                                                                                                                         44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-339965/46.
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                       82 AA;
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Ω 원 AAB01906;

AAB01906 RESULT

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inhibiting endothabilar call proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1, kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4 bRKLS protein The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop
    3 DCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDIN 62
                                4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence, human kringle 1, is a specific angiostatin fragment which can be used in the invention, and represents amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to new methods and compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies for use in diagnosis, detection and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 256.5; DB 1
Pred. No. 5.6e-18;
3; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin J, Oreilly MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 104; 203pp; English.
                                                                                                   83
                                                                                                                                                GPWCYTTDPEKRYDYCDILEC 83
                                                                                                                                                                                                                                                                   AAW07545 standard; protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids 6-84 of human angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                 63 GPWCYIMNPRKLFDYCDIPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0612788.
95US-0429743.
96US-0605598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US05856
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Folkman MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-518662/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               human kringle 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9635774-A2
                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1996
                                                                                                                                                                                                                                                                                                                  AAW07545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cao Y,
                                                                                                                                                                                                                                               AAW07545
                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphomas. They are also used for the prophylaxis of various autoimmune diseases (e.g., rheumatoid arthritis), ocular diseases, skin diseases (e.g., psoriasis), blood vessel diseases (e.g., haemangiomas, Osler-Webber Syndrome), diseases caused by excessive or abnormal stimulation of endothelial cells (e.g., Crohn's disease, atherosclerosis), diseases which have angiogenesis as a pathologic consequence (e.g., cat scratch disease and ulcers). The peptides are also useful as a birth control agent which inhibits ovulation and establishment of the placenta.

Sequences Aababa906-B01919 sepresent fragments of human plasminogen used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                        Plasminogen; human; kringle domain; endothelial cell proliferation; angiogenesis; antiproliferative; antiarteriosclerotic; cytostatic; antinflammatory; antiuloer; antirheumatic; antiarthritic; antiangiogenic; cancer; tumour; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method of preparing plasminogen kringle 5 peptide fragments. The method comprises mixing mammalian plasminogen and elastase in the ratio 1:100-1:300, followed by incubating and isolating the fragment. The kringle 5 peptides are inhibitors of anglogenesis and endothelial cell proliferation and migration. The peptides are useful for treating anglogenic diseases, primary and metastatic solid tumours and carcinomas of various organs such as breast, genital tract, endocrine glands, skin, tumours of the brain and eyes and solid tumours arising from haematopoietic malignancies such as leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: This sequence is not shown in the specification, but is derived from the full length human plasminogen sequence (AAB01887) shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of Kringle five peptide fragment for treating various disorders such as angiogenic, coular, skin diseases and cancer, involves mixing mammalian plasminogen and elastase followed by incubation and isolation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 258.5; DB 21; Length 8 Pred. No. 3.8e-18; 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                             Human plasminogen kringle 1 (Tyr80-Glu163).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 17; Page -; 48pp; English.
                                                                                                                                                               AAB01906 standard; Protein; 84 AA.
GPWCYTMNPRKLFDYCDIPLC 83
                        ||||||| :| | :||||| | GPWCYIIDPEKRYDYCDILEC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0643219.
97US-0832087.
                                                                                                                                                                                                                                                              18-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-349573/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davidson DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6057122-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000.
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63

17; Length 79;

27; Indels

Seguence

Query Match

figure 1.

RESULT 10 AAP90598

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The specification describes a human polypeptide which is a potent angiogenesis inhibitor, and is designated KBD. KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthirits, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome, Castleman's disease, psorhasis, hepetifits, ameurysm, renal disease and haemangioma. The present sequence represents kringle I of human plasminogen, which is used in the course of the invention.
                                                                                                    Angiogenesis inhibitor; KED; kringle protein; angiogenesis; tPA; tissue plasminogen activator; tumour; atherosclerosis; arthritis; retinopathy; bronchial vascular congestion; inflammatory bowel disease; adult respiratory distrass syndrome; Castleman's disease; psoriasis; hepatitis; aneurysm; renal disease; haemangioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.7%; Score 252.5; DB 21; Length 53.1%; Pred. No. 1.5e-17; tive 8; Mismatches 29; Indels
                                                                   Amino acid sequence of kringle 1 of human plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dou D, Chopp M, Wang L, Mikkelsen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 6; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPWCYTTDPEKRYDYCDTLEC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP81360 standard; protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GPWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                 (FORD-) FORD HEALTH SYSTEM HENRY.
                                                                                                                                                                                                                                                                                                                                                         99US-0121341.
99US-0121633.
99US-0166176.
                                                                                                                                                                                                                                                                                                                         24-FEB-2000; 2000WO-US04798
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(first entry)
                                 20-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-572016/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 AA;
                                                                                                                                                                                                                                                   WO200049871-A1.
                                                                                                                                                                                                                                                                                                                                                         24-FEB-1999;
25-FEB-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                     31-AUG-2000
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06-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81360;
AAB08410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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AAP81360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDIN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inserted in front of an N-terminal 1-82 AA truncated t-PA protein, new product has an increased affinity to fibrin. decreased reactivity with inhibitors and increased thrombolytic and fibrinolytic activity. (Updated on 31-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct DI field.)
                                                                                                                                                                                                                                                                                 Synthetic N-terminal protein of truncated human tissue plasminogen activator (t-PA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue plasminogen activator variants - having N-terminal domain replaced with first kringle region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 254; DB 10; Length 81;
Pred. No. 1e-17;
9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                      t-PA; tissue plasminogen activator; thrombolytic; fibrinolytic; fibrin; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Langersafe P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB08410 standard; Protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GPWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                       AAP90598 standard; protein; 81 AA
                                60 PWCYTTDPEKRYDYCDILEC 79
               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 32; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWCYTMNPRKLFDYCDIPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-US02263,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87US-0070012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0184121
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                 (updated)
                                                                                                                                                                                                                                (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain of plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larsen GR, Ahern T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-039648/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN91194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1987;
20-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1988;
                                                                                                                                                                                                             25-MAR-2003
31-OCT-2002
                                                                                                                                                                                                                                             13-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S:
               64
                                                                                                                                                                           AAP90598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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HAND BENEFIT OF SECOND OF

62

AAB08410 ID AAB0 XX RESULT 11

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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                              The kringle K1 domain (AAR96221) of plasminogen was incorporated into tissue plasminogen activator (tPA) (see also AAR96220) as a replacement for the native tPA kringle 1 sequence, producing a novel plasminogen activator (see also AAR96222). This was performed by insertion of plasminogen K1 DNA (AAR27786) into a native tPA sequence (AAF27585) and expression in Escherichia coli RRI transformants (FERM P-9272). Such protocols can be used to produce novel plasminogen activators that show increased clot lysing specificity or plasma half-life. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; fibrinolytic; t-PA; plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 79;
                                                                                                                                                                                               Hybrid plasminogen activator comprises human tPA activator an N-terminal crosslinking domain from alpha2-plasmin inhibitor useful to treat thrombosis and image blood clots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohara PJ, Nexo BA, Yoshitake S, Ikeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%; Score 251.5; DB 17; Length 53.8%; Pred. No. 1.7e-17; Indels 17ve 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding K1 domain of plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP94401 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||| :| :|||| | PWCYTTDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                  Example 3; Fig 4; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87JP-0058061
88JP-0062847
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                               92US-0827587.
               87US-0125629
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVO INDUSTI A/S.
(ZYMO ) ZYMOGENETICS INC.
(EISA ) EISAI CO LTD.
                                                                                  (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                WPI; 1996-187699/19.
N-PSDB; AAT27586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1987;
02-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-2002
18-JUN-1990
                               28-JAN-1992;
06-JUN-1994;
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                                                                                                                 Foster DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP94401;
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                                                                                                                                                                                                                                                                                                                                                                                                     New tissue plasminogen activator analogues with non-native K1-domain having higher fibrin specificity, and new encoding DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The KI domain of plasminogen may be used to replace the KI domain of t-PA to produce an analogue with greater specificity for fibrin than native t-PA.

(Updated on 31-OCT-2002 to add missing OS field.)

(Updated on 25-WAR-2003 to correct PA field.)

(Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue plasminogen activator; tPA, alpha2-plasmin inhibitor; fibrinolytic; thrombolytic; fibrin; thrombosis; blood clotting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 79;
                                                                                                                                                                                                                                                                                                   Yoshitake S, Ikeda Y, Suzuki S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 251.5; DB 9; Length Pred. No. 1.7e-17; 9; Mismatches 27; Indels
                                 Tissue plasminogen activator; analogue; Kl domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR96221 standard; Protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page ?; ?pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 PWCYTTDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasminogen kringle domain Kl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein engineering; kringle.
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                                                                                                                                                                                                 87US-0058217.
                                                                                                                                                                  88EP-0108949
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(first entry)
                                                                                                                                                                                                                                                                                                 Mulvihill ER, Nexo BA, 19 Hashimoto A, Yuzuriha T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 53.8 tes 43; Conservative
                                                                                                                                                                                                                               (ZIMO ) ZIMOGENETICS INC. (NOVO ) NOVO IND AS. (EISA ) EISA CO LID.
K1 domain of plasminogen
                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-347625/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA;
                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN81087
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06-AUG-1996
                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                        1 CKTGDGKNYRGIMSKTKNGITCQKWSSTSPHR-PRFSPATHPSEGLEENYCRNPDNDPG 59
                                                                                                                                    Amino acid sequence of kringle domain of plasminogen, incorporated into plasmid PKI. Sequence is derived from II synthetic oligonuclectides. Alternatively the sequence is described as encoding Asn at position 96. (Updated on 01-JUL-2002 to add missing PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to new methods and compositions for inhibiting endothelial cell proliferation, using as active component an angiostatin fragment, a combination of angiostatin fragments, or aggregate angiostatin. The fragment is preferably derived from murine, human, Rhesus, porcine or bovine plasminogen and is a kringle 1,
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis; macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of angiostatin fragments or aggregates - for inhibiting endothelial cell proliferation and treating angiogenesis-mediated diseases, e.g. cancer, arthritis or diabetic retinopathy
                                                                      the growth factor domain
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                                                                                                                                                                                                                         Score 248.5; DB 10; Length 78; Pred. No. 3.4e-17;
                                                                                                                                                                                                                                                   25; Indels
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                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Folkman MJ, Lin J, Oreilly MS,
                                                            Tissue plasminogen activator analogues having at least one cystine residue in replaced with another amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW07547 standard; protein; 79 AA.
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                                                                                                             Example 9; Fig 11; 95pp; English
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96US-0605598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                   42; Conservative
Hashimoto A, Yuzuhira T;
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Best Local Similarity
                        WPI; 1989-039773/06.
N-PSDB; AAN91218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine kringle 1.
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22-FEB-1996;
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kringle 2, kringle 3, kringle 2-3, kringle 1-3, kringle 1-2, kringle 1-4 or kringle 1-4BKLS protein. The aggregate angiostatin has a Mol. Wt. of 45-65 kD and is derived from a plasminogen fragment beginning at approximately amino acid number 98 of murine, human, Rhesus, porcine or bovine plasminogen. The active component can be used for treating angiogenesis:mediated diseases such as cancer, arthritis, macular degeneration and diabetic retinopathy. It can also be used to develop antibodies for use in diagnosis, detection and therapy. The present sequence, porcine Kringle 1, is a specific angiostatin acids 6-84 of porcine angiostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 246.5; DB 17; Length 79; Pred. No. 5.4e-17; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PWCYTTDPETRFDYCDIPEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                      ch 48.5%;
1 Similarity 53.8%;
43; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 79 AA;
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Sequence 6, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appli
Sequence 11, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
                                                                                    September 29, 2003, 08:45:34 ; Search time 29 Seconds
(without alignments)
125.474 Million cell updates/sec
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Sequence 2
Sequence 5
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508
1 BQDCMFGNGKGYRGKKATTV.....YTMNPRKLFDYCDIPLCASS
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-763-528A-1
US-08-612-788-9
US-09-066-028-9
US-09-066-028-11
US-09-33-325-9
US-09-35-325-11
US-09-35-325-11
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Listing first 45 summaries
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28 222 43.7 78 3 US-09-066-028-23 Sequence 23, Appl 30 222 43.7 78 4 US-09-335-325-17 Sequence 17, Appl 31 220 43.7 78 4 US-09-335-325-23 Sequence 16, Appl 32 20 43.3 78 2 US-08-612-788-16 Sequence 16, Appl 32 220 43.3 78 3 US-09-066-028-16 Sequence 16, Appl 32 220 43.3 78 3 US-09-066-028-16 Sequence 16, Appl 35 220 43.3 78 3 US-09-066-028-16 Sequence 16, Appl 36 220 43.3 78 3 US-09-066-028-16 Sequence 16, Appl 36 220 43.3 78 3 US-09-066-028-16 Sequence 16, Appl 37 217 42.7 78 2 US-08-612-788-12 Sequence 12, Appl 40 216 42.5 78 2 US-08-612-788-13 Sequence 12, Appl 41 216 42.5 78 2 US-08-612-788-14 Sequence 12, Appl 42 216 42.5 78 3 US-09-066-028-14 Sequence 13, Appl 44 216 42.5 78 3 US-09-066-028-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-13 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 3 US-09-066-028-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14 Sequence 14, Appl 45 216 42.5 78 4 US-09-335-325-14
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Sequence 6, Application US/08763528A

Patent No. 5854221
GENERAL INFORMATION:
APPLICANT: FOLKman, M. Judah
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,528A
FILING DATE: 12-DSC-1996
CLASSIFICATION: 530
                                                                                                                                                                          SSEE: Jones & Askew, LLP
1: 191 Peachtree Street, 37th Floor
Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Kringle 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0251
TRIECOMMUNICATION INFORMATION:
TRIEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

'TOWATTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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STREET: 19
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                  US-08-763-528A-6
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STATE:
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RESULT 1
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Length 80;

DB 2;

Score 412;

81.18;

Query Match

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CITY: Atlanta
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                                                            4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                 1 CMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGG 60
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                       Gaps
                                                                                                                                                                                                                                                       Sequence 1, Application US/08763528A;
Sequence 1, Application US/08763528A;
Patent No. 585421
GENERAL INFORMATION:
APPLICANT: Cao, Yihai
APPLICANT: CAC, Yihai
TITLE OF INVENTION: Endothalial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF ENGURNES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
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Pred. No. 5.7e-39;
5; Mismatches 7; Indels
Pred. No. 9.3e-40;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFRAME: IBM PC compatible
SOFRAME: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,528A
FLING DATE: 12-20-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Jones & Askew, LLP STREET: 191 Peachtree Street, 37th Floor CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: WARTEN, WALLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0251
TELECHOMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
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US-08-612-788-9
; Sequence 9, Application US/08612788
                                                                                                                                                             61 PWCYTTNPRKLYDYCDVPOC 80
                                                                                                                                          64 PWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.7%;
Best Local Similarity 84.6%;
Matches 66; Conservative 5
  Best Local Similarity 83.8%;
                       67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georgia
: US
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                                                                                                                                                                                                                                        RESULT 2
US-08-763-528A-1
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COUNTRY:
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
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Patent No. 6024688
GENERAL INFORMATION:
APPLICANT: FOLKAIN, M. Judah
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
GENERAL INFORMATION:

APPLICANT: FOlkman, M. Judah

APPLICANT: O'Reilly, Micheal

APPLICANT: Cao, Yiha

APPLICANT: Sim, B. Kim Lee

APPLICANT: Sim, B. Kim Lee

NUMBER OF SINUBNICES: 45

CORRESPONDENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.0%; Score 274.5; DB 2; Length 79; 58.8%; Pred. No. 3.9e-24; Live 8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                   COMPUTER: SUCCESSION OF A COMPUTER: SUCCESSION OF A COMPUTER: TBM PC COMPUTER: DECESSION OF THE COMPUTER: DECESSION OF THE COMPUTER: DECESSION OF THE COMPUTER: DECESSION OF THE COMPUTER OF THE CATION NUMBER: US/08/612,788

FILING DATE: TROUBLER: SIGNATION: NAME: WALTEN WALTEN WALTEN WILLIAM L.

REGISTRATION NUMBER: 36,714

REGISTRATION NUMBER: 36,714

REGISTRATION NUMBER: 36,714

RELEPHONE: 404,818-7700
                                                                                                                                                                                                E: Jones & Askew
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||| :| : ||||||| |
60 PWCYTIDPEERFDYCDIPEC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rhesus monkey
IMMEDIATE SOURCE:
CLONE: K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Folkman, M. Judah
APPLICANT: Polkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnes & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-7un-1999
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.0%; Score 274.5; DB 4;
58.8%; Pred. No. 3.9e-24;
tive 8; Mismatches 24;
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788
FILIND DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:

NAME: WATTEN, William L.

REGISTRATION NUMBER: 35,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELEPHONE: 404-818-3799

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 79 aming acids
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ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rhesus monkey
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 PWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.8
Matches 47; Conservative
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STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
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US-08-612-788-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 54.0%; Score 274.5; DB 3; Length 79; Best Local Similarity 58.8%; Pred. No. 3.9e-24; Matches 47; Conservative 8; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                 SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,028
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STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/612,788
FILING DATE:
APPLICATION NUMBER: 08/612,788
FILING DATE:
APPLICATION NUMBER: 05.114
REGISTATION NUMBER: 36,714
REPRENCE/DOCKET NUMBER: 05.213-0126
TELECOMMUNICATION INFORMATION:
TELEFRA: 404-618-3709
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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US-09-335-325-9
S-09-335-325-9
S-09-335-9
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COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rhesus monkey IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                ZIP: 30303-1769
                                                                       Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                   Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
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                                                                                                    COUNTRY:
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
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Patent No. 6521439
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
O'Reallly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 79;
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OPERATING STETEM: PC-DOS/MS-DOS
OPERATING STETEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOWEER: US/09/335,325
FLING DATE: 17-Jun-1999
CLASSIFICATION: <URKNOWN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,786
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 PWCYTTDPDKRYDYCDIPEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 PWCYTMNPRKLFDYCDIPLC 83
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 404-818-3799 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:

ORIGINAL SOURCE:

ORIGINAL SOURCE:

IMMEDIATE SOURCE:

CLOME: K1
US-09-066-028-11
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                                                                                                LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-335-325-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 258.5; DB 2; Length 79;
Pred. No. 2.6e-22;
7; Mismatches 26; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                          NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05213-0126
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09066028
Patent No. 6024688
GENERAL INFORMATION:
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STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRP PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| :| | :|||||| | 60 PWCYTTDPDKRYDYCDIPEC 79
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NAME: Warren, William L.
REGISTRATION UNDERS: 36,714
REFERENCE/DOCKET NUMBER: 0521:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%;
                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                             LENGTH: 79 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IMMEDIATE SOURCE:
; CLONE: K1
US-08-612-788-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N
ORIGINAL SOURCE:
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ON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
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APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 256.5; DB 2; Length 79;
Pred. No. 4.4e-22;
8; Mismatches 27; Indels
                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDEPPY disk
COMPUTER: IMP PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/612,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
FILING DATE: 12-DEC-1996
                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WARLEN, WAILHAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECHANTICALION INFORMATION:
TELEPHONE: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Sequence 2, Application US/08763528A
; Patent No. 5854221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PWCYTTDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.5%;
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                               79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 44; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-763-528A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-612-788-8
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                                                                                                                                                                                                                                                                                                                                3 DCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDIN 62
                                                                                                                                                                                                                                                                        Gaps
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Fatent No. 5837682
GENERAL INFORMATION:
FAPPLICANT: FOLKman, M. Judah
APPLICANT: Co, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCES. 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09348953
; Patent No. 6538103
; GENERAL INFORMATION:
; APPLICANT: Ji, Richard Wei-Dong
; APPLICANT: Trail, Penmela A.
; TITLE OF INVENTION: LYSINE BINDING FRAGMENTS OF ANGIOSTATIN
; FILE REPERENCE: DB11Sequences
; CURRENT FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/092,831
; PRIOR FILING DATE: 1998-07-14
; NUMBER: OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO :
; SEQ ID NO :
                                                                                                                                                                                                                              DB 4; Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 258.5; DB 4; Length 8 Pred. No. 2.7e-22; 9; Mismatches 27; Indels
                                                                                                                                                                                                                            Query Match 50.9%; Score 258.5; DB 4; Length Best Local Similarity 57.5%; Pred. No. 2.6e-22; Matches 46; Conservative 7; Mismatches 26; Indels
                                                                                                                                              CLONE: K1
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 GPWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                                                                                                                                                                                                                                                                                              64 PWCYTMNPRKLFDYCDIPLC 83
                                                            FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.9%;
Best Local Similarity 54.3%;
Matches 44; Conservative
MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                    ORGANISM: Bovine IMMEDIATE SOURCE:
                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 191 P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: human
US-09-348-953-1
                                                                                                                                                                                      US-09-335-325-11
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US-09-348-953-1
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Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
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ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 PWCYTTDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09335325
Patent No. 6521439
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: HOMO sapiens IMMEDIATE SOURCE: CLONE: K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 8:
                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
TYPE: amino acid
                                                                                     TYLE:
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.03
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
      404-818-3799
                                                                                                                                                                                    ANTI-SENSE: NO
      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-335-325-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CKTGNGKNYRGTMSKTKNGITCQKWSSTSPHR-PRESPATHPSEGLEENYCRNPDNDPQG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOLKMan, M. Judah
APPLICANT: O'Reilly, Micheal
APPLICANT: O'Reilly, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Cao, Yihai
APPLICANT: Sin, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ) LOCATION: 1..79
) OTHER INFORMATION: /note= "Kringle 1 - Figure 3"
US-08-763-528A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/066,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 256.5; DB 2;
Pred. No. 4.4e-22;
8; Mismatches 27;
          ATTORNEY ACENT INFORMATION:
NAME: Warren, William L.
REGIERATION NUMBER: 36,714
REPRENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEPAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren, William L.
REGISCRRATION NUMBER: 36,714
REGISCREPRENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAUE: Georgia
COUPTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: LEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PWCYTYDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/09066028; Patent No. 6024688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.5%;
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                                                                                                                                                                                               LENGTH: 79 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.09
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                           8
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ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-066-028-8
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                               APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                       μ;
50.5%; Score 256.5; DB 3; Length 79; 55.0%; Pred. No. 4.4e-22; tive 8; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT IN PROTOCOMPATION COMPOURE: ISM PC COMPATION CONTRACTOR SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DAM:

APPLICATION NUMBER: US/09/335,325 FILING DATE: 17.5un-1999 CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
RPLICATION DATA:
APPLICATION NUMBER: US/08/612,788 FILING DATE: CURROWN>
ATORNEY/AGENT INFORMATION:
NAME: WATFOR WIlliam I.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 36,714
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4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                             4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                   Gaps
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APPLICANT: Folkman, M. Judah
APPLICANT: O'SHILLY, Micheal
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnes & Askew
STREET: 191 Peachtree Street, 37th Floor
                       Length 79;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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APPLICATION NUMBER: US/09/066,028 FILING DATE:
                    48.5%; Score 246.5; DB 2;
53.8%; Pred. No. 6e-21;
tive 7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.5%; Score 246.5; DB 3; Best Local Similarity 53.8%; Pred. No. 6e-21; Matches 43; Conservative 7; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISFRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE; Georgia
COMPRT: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IB PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/09066028
; Patent No. 6024688
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APPLICATION NUMBER: 08/612,788
FILING DATE:
                                                                                                                                                                                    64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                           60 PWCYTIDPETRFDYCDIPEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal
                    Query Match
Best Local Similarity 53.88
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: K1
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US-09-066-028-10
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                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08612788
Patent No. 5837682
GENERAL INFORMATION:
FAPLICANT: FOLKman, M. Judah
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Anglostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                   Query Match 50.5%; Score 256.5; DB 4; Length 79; Best Local Similarity 55.0%; Pred, No. 4.4e-22; Matches 44; Conservative 8; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PartentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELEPHONE: 404-818-3700
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARLES:
                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Homo sapiens IMMEDIATE SOURCE: CLONE: K1
                                                                                                                                                                                                                                                                                                                                                                                  64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                         60 PWCYTIDPEKRYDYCDILEC 79
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 79 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-ter
ORIGINAL SOURCE:
ORGANISM: Porcine
                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.
ZIP: 30303-1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IMMEDIATE SOURCE:
; CLONE: K1
US-08-612-788-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-612-788-10
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Search completed: September 29, 2003, 08:50:31 Job time: 29 secs

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508
1 BQDCMFGNGKGYRGKKATTV.....YTMNPRKLFDYCDIPLCASS
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566894 seqs, 151307093 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
                                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 6, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 47, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 7, Appli	
ID	US-09-753-064-6	US-10-267-137-8	US-09-753-064-1	US-09-761-120-47	US-09-761-120-9	US-09-335-325-9				US-10-131-241-11					US-10-131-241-8
rth DB	80 9	80 12	6 6/	6 08	79 9	79 10	79 15			79 15					79 15
% Query Match Length DB	81.1	81.1	79.7	76.2	54.0	54.0	54.0	50.9	50.9	50.9	50.5	50.5	50.5	50.5	50.5
Score	412	412	405	387	274.5	274.5	274.5	258.5	258.5	258.5	256.5	256.5	256.5	256.5	256.5
Result No.	1	7	m	4	ហ	9	7	80	თ	10	11	12	13	14	15

Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 7, Appl Sequence 22, Appl Sequence 22, Appl Sequence 21, Appl Sequence 10, Appl Sequence 11, Appl Sequence 17, Appl Sequence 16, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 11,	eration inhibitor or #1.30
US-09-761-120-10 US-09-335-325-10 US-09-335-325-10 US-09-335-325-7 US-09-761-120-22 US-09-761-120-22 US-09-761-120-7 US-09-761-120-7 US-09-761-120-7 US-09-761-120-7 US-09-761-120-7 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-17 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-10 US-09-761-120-12 US-09-761-120-12 US-09-761-120-12 US-09-761-120-12	LIGNMENTS LIGNMENTS al Cell Prolif of of Use ", LLP reet, 37th Flo the columnation of Use ", TLP 09/753,064 0
24444444444444444444444444444444444444	a.064-6 ce 6, Application US/09753064 No. US200100156441 RAL INFORMATION:
8986	3-064-6 Tee 6, Application No. US20010016644 No. US20010016644 TITLE OF INVENTIO NUMBER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: 191 STREET: 191 STREET: 191 STREET: 30303 COMPUTER READABLE MEDIUM TYPE: COMPUTER READABLE COMPUTER READABLE MEDIUM TYPE: COMPUTER: 192 SOFTWARE: PA COMPUTER: 194 SOFTWARE: PA TELEPROMUNICATION TELEPROMUNICATION TELEPROMUNICATION SECRETARION FOR SEQ ID SEQUENCE CHARACTE
2444 64444 654444 65	TT 1 Guence 6, App tent No. US20 GENERAL INFOR TITLE OF NUMBER O CORRESPO CORRESPO COMPUTER MED COM OPE SOF CURREN COM OPE SOF COM OPE SOF CURREN COM OPE SOF COM
HHHHGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 1 US-09-753- Sequence Patent N GENERA A A A A A A A A A A A A A A A A A A

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GENERAL INFORMATION:
APPLICANT: Cao, Yihai
                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                           ZIP: 30303
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                                                                                                                                                                                                                                                                                                                                                                                                               1 CMFGNGKGIRGKRAITVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGG 60
                                                                                                                                                                                                                                                                                                                                                                                        4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Sequence alignment of kringle domains of ; OTHER INFORMATION: plasminogen and HGF US-10-267-137-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10267137
Sequence 8, Application US/10267137
Publication No. US20030148950a1
GENERAL INFORMATION:
APPLICANT: Li, Zai-Ping
APPLICANT: Li, Zai-Ping
APPLICANT: Au, Ren-bao
APPLICANT: Xu, Ren
TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
FILE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
FILE REPERENCE: 24282000100
CURRENT APPLICATION NUMBER: US/10/267,137
CURRENT APPLICATION NUMBER: 60/328,329
PRIOR FILING DATE: 2001-10-09
                                                                                                                                                                                                       LOCATION: 1..80
OTHER INFORMATION: /note= "Kringle 5 - Figure 3"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                   81.1%; Score 412; DB 9; Length 80;
83.8%; Pred. No. 6.5e-39;
Live 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.1%; Score 412; DB 12; Best Local Similarity 83.8%; Pred: No. 6.5e-39; Matches 67; Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGIH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PWCYTINPRKLYDYCDVPQC 80
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; Patent No. US20010016644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PWCYTTNPRKLYDYCDVPQC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PWCYTMNPRKLFDYCDIPLC 83
LENGTH: 80 amino acids
                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE: internal
                                                                                                                                                                                    NAME/KEY: Protein
                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 83.8 Matches 67; Conservative
                                                                                                                                                                 FEATURE
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US-09-753-064-1
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Sequence 47, Application US/09761120

Patent No. US20020037847A1

GENERAL INFORMATION:

PAPLICANT: FOLKMEN, M. Judah

APPLICANT: O'Rellly, Michael

TITLE OF INVENTION: Nucleic Acids. Encoding Kringle 1-5 Region Fragments of Plasmin

FILE REFERENCE: 05940-0151 (43171-252068)

CURRENT PELING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US/09/761,120

CURRENT PILING DATE: 1999-05-11

PRIOR FILING DATE: 1999-05-11

PRIOR FILING DATE: 1999-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CMFGNGKGYRGXKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
FOLKman, M. Judah
TITLE OF INVENTION: Endothelial Cell Proliferation Inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 405; DB 9; Length 79; Pred. No. 3.9e-38; Mismatches 7; Indels
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PR-FC-FOS/NS-FOS
SOFFWARE: Patentin_Release #1.0, Version #1.30
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
SIREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0251
TELECOMMUNICATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/763,528
FILING DATE: 12-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PWCYTTNPRKLYDYCDVP 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.7%;
Best Local Similarity 84.6%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                    CITY: Atlanta
STATE: Georgia
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Sequence 9, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prol
TITLE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/11,241
CURRENT FILING DATE: 2002-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 274.5; DB 10; Length 79; ilarity 58.8%; Pred. No. 1.7e-23; Conservative 8; Mismatches 24; Indels 1;
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
                                             ADDRESSEE: Jones & Askew STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <UDKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 PWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                      CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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Best Local Similarity
Matches 47; Conserve
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US-10-131-241-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FOLKAIN, M. Judah
APPLICANT: FOLKAIN, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Muchael Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
FILE REFERENCE: 05940-0151 (43171-252068)
CURRENT APPLICATION NUMBER: U5/09/7/61,120
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CKTGNGKNYRGTMSKTRTGITCQKWSSTSPHR-PTFSPATHPSEGLEENYCRNPDNDGQG 59
                                                                                                                                                                                                                                                                                                                                               4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Angiostatin Fragments and Method of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 79;
                                                                                                                                                                                                                                                 Score 387; DB 9; Length 80;
Pred. No. 4.2e-36;
3; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/30/761,1
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1099-05-11
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR PLING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 9
LENGTH: 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Folkman, M. Judah
O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PWCYTYNPRKLYDYCDIPLC 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 PWCYTMNPRKLFDYCDIPLC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 PWCYTMNPRKLFDYCDIPLC 83
NUMBER OF SEQ ID NOS; 47
SOFTWARE: PatentIn version 3.0
SEQ ID NO 47
                                                                                                                                                                                                                                                    Query Match 76.2%;
Best Local Similarity 80.0%;
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Kringle 1
                                                                                                                                                         ) NAME/KEY: misc_feature
; OTHER INFORMATION: Kringle 5
US-09-761-120-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.8
Matches 47; Conservative
                                                                                             TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Macaca sp.
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US-09-761-120-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-335-325-9
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                                                                                                                                        FEATURE
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RESULT 10
19-10-131-241-11
1 Sequence 11. Application US/10131241
2 Sequence 11. Application US/2030012792A1
3 Fublication No. US20030012792A1
3 GENERAL INFORMATION:
3 APPLICANT: Holaday, John W.
4 APPLICANT: Fortier, Anne H.
5 TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
5 FILE REPERENCE: OS13-0-34 4 43170-271565
5 CURRENT APPLICATION NUMBER: US/20/10/131,241
5 CURRENT FILING DATE: 1999-10-06
6 PRIOR FILING DATE: 1999-10-06
6 PRIOR FILING DATE: 1999-05-21
6 PRIOR APPLICATION NUMBER: US 60/086,586
7 PRIOR APPLICATION NUMBER: US 60/086,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CMFGNGKGYRGKKATIVIGIPCQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                          COMPUTER READABLE FORM:

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 11-Jun-1999

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                               STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 50.9%; Score 258.5; DB:
Local Similarity 57.5%; Pred. No. 1.1e-21
nes 46; Conservative 7; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warren, William L.
REGIGTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

**PAPLICATION NUMBER: US/08/612,788
**FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                         & Askew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PWCYTTDPDKRYDYCDIPEC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 79 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                               CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: K1
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Best Local Si
Matches 46;
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TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminoge
TITLE REFERENCE: 05940-0131 (43171-252068)
CURRENT APPLICATION NUMBER: U5/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                     4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
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                                                                                                                                                                                                                                                                            Gaps
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O'Reilly, Micheal
Cao, Yihai
Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                          Ή,
                                                                                                                                                                                                                             Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 50.9%; Score 258.5; DB 9; Length 79; Best Local Similarity 57.5%; Pred. No. 1.1e-21; Matches 46; Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                           Score 274.5; DB 15; Length
Pred. No. 1.7e-23;
8; Mismatches 24; Indels
PRIOR APPLICATION NUMBER: US 60/086,586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09761120
Patent No. US20020037847A1
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
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60 PWCXTIDPEERFDXCDIPEC 79
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SOFWHARE: Patentin version 3.0
SEQ ID NO 179
LENGTH: 79
                  PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFWMARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 79
                                                                                                                                                                                                                             54.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEX: misc_feature; OTHER INFORMATION: Kringle 1
US-09-761-120-11
                                                                                                                                                                                                                                                                          47; Conservative
                                                                                                                                      TYPE: PRT
ORGANISM: Rhesus monkey
                                                                                                                                                                                                                             Query Match
Best Local Similarity
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US-09-761-120-11
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APPLICANT: Folkman, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: NUCLEIC ADDISONATION TO RELEASE
TITLE REFERENCE: 05940-0151 (43171-255068)
CURRENT APPLICATION NUMBER: 05/09/761,120
CURRENT FILING DATE: 2001-01-16
PRIOR PPLICATION NUMBER: 09/309,821
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR APPLICATION NUMBER: 08/866,735
PRIOR FILING DATE: 1997-05-30
                                                                                                                                   4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                          1 CKTGNGKNYRGTMSKTKNGITCQKWSSTSPHR-PRESPATHPSEGLEENYCRNPDNDPQG 59
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Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
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                                                                                              Indels
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STREET: 191 Peachtree Street, 37th Floor
                                                    Score 256.5; DB 9;
Pred. No. 1.8e-21;
8; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 256.5; DB 9;
Pred. No. 1.8e-21;
8; Mismatches 27;
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                                                                                                                                                                                                                                        60 PWCYTTDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09761120 Patent No. US20020037847A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09335325; Patent No. US20020164717A1
GENERAL INFORMATION:
                                                                                                                                                                                                                 64 PWCYTMNPRKLFDYCDIPLC 83
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O'Reilly, Micheal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
ERNOTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.5%;
Best Local Similarity 55.0%;
Matches 44; Conservative
                                                      50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; OTHER INFORMATION: Kringle 1
US-09-761-120-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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ZIP: 30303-1769
COMPUTER READABLE FORM:
                                                      Query Match
Best Local Similarity 55.0°
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-09-335-325-8
              US-09-753-064-2
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                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Folkman, M. Judah

IIILE OF INVENTION: Endothelial Cell Proliferation Inhibitor and Method of Use
                                                                                                                                                                                        Score 258.5; DB 15; Length 79; Pred. No. 1.1e-21; 7; Mismatches 26; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/753,064
FILING DATE: 29-Dec-2000
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/763,528

FILING DATE: 12-DEC-1996

ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REGISTRATION NUMBER: 36,714

RELECHOMENICATION INFORMATION:
TELEPHONE: 404-818-3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                         60 PWCYTTDPDKRYDYCDIPEC 79
                                                                                                                                                                                                                                                                                                                                                  64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09753064 Patent No. US20010016644Al
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LENGTH: 79 amino acids
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INFORMATION FOR SEQ ID NO: 2:
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STRANDEDNESS: single
                         NUMBER OF SEQ ID NOS: 65
SOFWRARE: Patentin version 3.1
SEQ ID NO 179
                                                                                                                                                                                      50.9%;
ilarity 57.5%;
Conservative
PRIOR FILING DATE: 1998-05-22
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FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Cao, Yihai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
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                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                          ; TYPE: PRT
; ORGANISM: Bovine
US-10-131-241-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-753-064-2
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MIN. Li
APPLICANT: MIN. Li
APPLICANT: Li, Zai-Ping
APPLICANT: Gan, Ren-bao
APPLICANT: Can, Qing-wei
APPLICANT: Can, Ren-bao
APPLICANT: Can, Qing-wei
TITLE OF INVENTION: KRINGLE DOMAIN 1 OF HUMAN HEPATOCYTE
TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
TITLE OF INVENTION: GROWTH FACTOR AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/10/267,137
CURRENT APPLICATION NUMBER: 60/328,329
PRIOR RELING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 13
SEQ ID NOS: 13
SEQ ID NO 7
LENGTH: 79
LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.5%; Score 256.5; DB 10; Length Best Local Similarity 55.0%; Pred. No. 1.8e-21; Matches 44; Conservative 8; Mismatches 27; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION WUMBER: US/08/612,788
FILING DATE: <UNANOWN-
ATTORNEY/AGENT INFORMATION:

NAME: WATTEN, William L.

REGISTRATION UNMBER: 36,714
REFERENCE/DOCKET WUMBER: 05213-0126
TELEPONE: 404-818-3700
TELEPAN: 404-818-3799
INFORMATION PO: B: 10 PO: 8: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 79 aming acids
                                                                                                                        APPLICATION NUMBER: US/09/335,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                           FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWCYTTDPEKRYDYCDILEC 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-267-137-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-335-325-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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RESULT 15

US-10-131-41-8

Sequence 6, Application US/10131241

Sequence 6, Application World 15241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell ProlifITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

FILER REFERENCE: 05213-0344 43170-271565

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR PRILING DATE: 1999-06-21

PRIOR PRILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LEMATH: 79

LEMATH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                              4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING 63
                                                                                                                                                                                  4 CMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDING
                                                                                                                   Gaps
                                                                                                                1,
                                                                   Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 79;
                                                                                                                27; Indels
                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 256.5; DB 15;
Pred. No. 1.8e-21;
8; Mismatches 27;
                                                                      Score 256.5; DB 1
Pred. No. 1.8e-21;
8; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 29, 2003, 08:59:02
Job time : 64 secs
; OTHER INFORMATION: plasminogen and HGF US-10-267-137-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 PWCYTYDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                               64 PWCYTMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                     60 PWCYTIDPEKRYDYCDILEC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.5%;
Similarity 55.0%;
44; Conservative 8
                                                                      Query Match 50.5%;
Best Local Similarity 55.0%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens US-10-131-241-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 44; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model protein search, OM protein -

September 29, 2003, 08:44:24; search time 39 Seconds (without alignments) 212.064 Million cell updates/sec Run on:

US-10-088-548-8 508 1 EQDCMFGNGKGYRGKRATTV......YTMNPRKLFDYCDIPLCASS Perfect score: Sequence:

86

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

96168682 residues 283308 seqs, Searched:

29185 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 86

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

pirl:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	neurotoxin V - Edv	hypot	neurotoxin V - sco	hypothetical prote		Ξ	glycoprotein H - h	hypothetical prote			₽	hypothetical prote			-4		a	glycoprotein H - h	glycoprotein H - h	hypothetical prote	ĸ,	hypothetical prote		_		Н	embryoqenic callus	-	
SUMMARIES	ΩĨ	NTSR5L	E82078	NTSR5M	T03082	G82600	NTSREB	PQ0852	T35510	S21332	D81186	TGEP5J	AF2564	AF3350	A69034	F83824	T17313	A34768	PQ0850	PQ0848	AE2406	S67923	E97800	E82529	T02631	G64561	94	T14285	35	30
	BB	-	7	Н	7	7	Н	7	7	7	7	Н	~	7	7	N	~	a	7	0	~	N	7	~	C)	~	~	N	(1)	7
	Length	64	65	64	65	9	65	65	40	59	29	59	77	51	62	73	86	71	9	65	65	46	80	20	62	62	64	69	74	82
о¥	Query Match		10.7	10.3			9.5		9.4	9.4				9.5					0.6	•	•	•	•			•	8.7	٠		
	Score	4	54.5	$^{\circ}$	51	σ	ä	48.5	4	٠	47.5	47	4	46.5	ė.	9	46.5	-17	45.5	ď.	•	45	45	₹.	44.5	44	44		44	44
	Result. No.	Н	7	m	4	Ŋ	ø	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	probable cold shoc	molybdopterin conv	hypothetical prote	hômeotic protein c	gp51 protein - Myc	hypothetical profe	high potential iro	50S ribosomal prot	hypothetical prote	intestinal trefoil	class II histocomp	hypothetical prote	hypothetical prote
2 F82496	2 \$70093						2 H72805	2 H84256		2 F84303					
8.7 86	9	9	. 9	8.6 86	ω.	ις.	8.5 65	8.5 74	٠. د	8.4 58	4	4	4	en	m
44	43.5	43.5	43.5	43.5	43	43	43	43	43	42.5	42.5	42.5	42.5	42	42
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
RESULT 1
```

neurotoxin V - Egyptian scorpion

C;Species: Leiurus quinquestriatus (Egyptian scorpion) C;Date: 30-Apr 1979 #sequence_revision 13-Jul-1981 #text_change 15-oct-1996

C; Accession: A01741

R;Kopeyan, C.; Martinez, G.; Rochat, H.
FEBS Lett. 89, 54-58, 1978
A;Title: Amino acid sequence of neurotoxin V from the scorpion Leiurus quinquestriati
A;Reference number: A01741; M0ID:78191225; PMID:658402
A;Note: L. q. quinquestriatus
A;Accession: A01741

A; Molecule type: protein A; Residues: 1-64 < KOP> C; Superfamily: socrpion neurotoxin C; Superfamily: socrpion neurotoxin C; Reywords: blocked carboxyl end; neurotoxin; venom F;12-63;16-36,22-46,26-48/Disulfide bonds: #status predicted F;64/Modified site: blocked carboxyl end (Asn) (probably amidated) #status experimen

11; DB 1; Length 64; Indels 15; 10.7%; Score 54.5; DB 34.0%; Pred. No. 49; iive 5; Mismatches Query Match 10.77 Best Local Similarity 34.0° Matches 16; Conservative

ä

35 RHSTFIPGTN-----KWAGLEKNYCR--NPDGDINGPWCXTMNPR 72 QY

54 10 KNCTFFCGRNAYCNDECKKKGGESGYCQWASPYG--NACWCYKLPDR g

RESULT 2 E82078

conserved hypothetical protein VC2429 [imported] - Vibrio cholerae (strain N16961 se. C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82078

RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller: I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301

A; Accession: E82078

A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-65 < HEI>
A; Cross-references: GB: AE004312; GB: AE003822; NID: 99656995; PIDN: AAF95572.1; GSPDB: GI
A; Experimental source: serogroup O1; strain N16961; biotype E1 Tor

A; Map position: 1

DB 2; Length 65; Score 54.5; I Pred. No. 50; 10.7%; 31.7%; Query Match Best Local Similarity

```
AjExperimental source: strain 9a5c
R;Simpson, A.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Remper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Le
chado, M.A.; Madelra, A.M.B.N.; Madelra, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A; Athlones: de Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: A01746
R;Martin, M.F.; Rochat, H.
Rydrin, 279-291, 1984
A;Title: Purification of thirteen toxins active on mice from the venom of the North A A;Reference number: A94316; MOID:84224814; PMID:6729843
A;Accession: A01746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence analyses of laborat
                                                                                                                                                        A;Cross-references: GB:AE004025; GB:AE003849; NID:g9107217; PIDN:AAF84897.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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C;Species: human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: PQ0852; PQ081; PQ0884; PQ0853
R;Gompels, U.A.; Carrigan, D.R.; Carss, A.L.; Arno, J.
J. Gen. Virol. 14, 613-622, 1993
A;Title: Two groups of human herpesvirus 6 identified by sequence analyses of A;Reference number: JQ2382; MUID:93224882; PMID:8385692
A;Reference number: JQ2382; MUID:93224882; PMID:8385692
A;Residues: 1-65 <GGM>A;Residues: 1-65 <GGM>A;Experimental source: strain C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Buthus occitanus tunetanus
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 23-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: neurotoxin; venom F;12-63,16-36,22-46,26-48/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 RHSTFIPGTNKWAGL-----EKNYCRNPDGDINGPWCYTM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 WCYTMNPR-----KLFDY-----CDIPLCAS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.5; DB 1;
Pred. No. 2.2e+02;
5; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.5; DB 2;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotoxin XI - scorpion (Buthus occitanus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%;
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Best Local Similarity 28.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-65 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                         A; Molecule type: DNA
A; Residues: 1-68 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation
                             A; Accession: G82600
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: XF2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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NTSREB
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Androctonus mauretanicus.
Cispecies: Androctonus mauretanicus.
Cipate: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 15-Oct-1996
Cipate: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 15-Oct-1996
Cipate: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 15-Oct-1996
Cipate: 15-Oct-1985 #sequence_revision 15-Oct-1982 #text_change 15-Oct-1996
Cipate: 1995 #sequence_revision of ten proteins from the venom of the Moroccan scorpion Androccan and Argentence number: A04318 MUID: 83193276; PMID: 3992595
Air Accession: A0174
Air Molecule type: protein
Air Molecule type: protein
Air Molecule type: protein
Air Molecule type: protein
Air Modified carboxyl end; neurotoxin; venom
Cireywords: blocked carboxyl end; neurotoxin; venom
Cireywords: blocked carboxyl end; neurotoxin; probably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 A;Reference number: 214834; MVID:98141693; PMID:9482589
A;Accession: T03082
A;Attaus: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-65 < EAH>
A;Cross-references: EMBL:AF003534; NID:92738385; PIDN:AAB94456.1; PID:92738429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: G82600
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;ittle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                  15 KKATTVTGTPC---QEWAAQEPHRHSTFIPGTNK-----WAGLEKNYCRNPDGDIN 62
                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appointment of protein 065L - Chilo iridescent virus C; Species: Chilo iridescent virus C; Species: Chilo iridescent virus C; Date: 24-Mar-1999 #text_change 08-Oct-1999 C; Accession: T03082 R; Bahr, U; Tidona, C.A.; Darai, G. Virus Genes 15, 235-245, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Xylella fastidiosa
;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                          3 KKLTIVKCPRCGTDVEWGEQSPHR----PFCSKQCQMIDFGEWADEEKAIPGAPDMSDS
   17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein XF2098 (imported) - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 FIPGTNKWAGLEKNYCRNPDGDINGPWCY------TMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.0%; Score 51; DB 2; Length 65; 29.1%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 TFIPGTN-----KWAGLEKNYCR--NPDGDINGPWCYTMNPR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                    neurotoxin V - scorpion (Androctonus mauretanicus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 52.5; D
36.4%; Pred. No. 81;
Live 3; Mismatches
   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 36.4
Matches 16; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                            63 GPW 65
                                                                                                                                                                                                                                                     DGW 60
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   Matches
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mambin - eastern Jameson's mamba
Milternate names; Milternate name; Milternate names; Milternate names
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A.Title: (1)H-NMR assignments and secondary structure of dendroaspin, an RGD-contain. A. Reference number: S50910; MuID:95112851; PMID:7813476
A. Accession: S50910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rifetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Accession: D81186
                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein NMB0542 [imported] - Neisseria meningitidis (strain MC58 serogro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:AE002098; NID:g7225766; PIDN:AAF40971.1; PID:g72:
B, strain MC58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-15, CT', 18-27, 'RNI', 28-32,34-59 <JOU>
C; Comment: The cell attachment motif may serve in inhibiting platelet aggregation.
C; Superfamily: snake toxin
C; Keywords: toxin; venom
F; 43-45/Region: cell attachment (R-G-D) motif
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81186
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                   Gaps
         11;
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                                                                                                                                                          22 GTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCR-NPDGDINGPW 65
         Indels
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A; Residuas: 1-59 <MCD>
A; Cross-references: PIDN:AAB2225.1; PID:g249694
A; Experimental source: venom
A; Experimental source: venom
A; Note: sequence extracted from NCBI backbone (NCBIP:104347)
         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.5; DB 2;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Scor
29.0%; Pred. No. 2...
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 PGNEOWNGHPRVFLPLCEGESGSVACPYCGT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PGINKWAGLEKNY -- - CRNPDGDINGPWCYT 68
              Mismatches
                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:AE002410;
A; Experimental source: serogroup
         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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Best Local Similarity
Matches 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-67 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: NMB0542
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              Matches
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submitted to the EMBL Data Library, October 1990
A; Description: Limited host range Ti plasmids; recent origin from wide host range Ti pla
A; Reference number: S21331
A; Accession: S21332
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dypothetical protein SC6G10.01c - Streptomyces coelicolor (fragment)
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Accession: T35510
R; Sceger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
A; Reference number: Z21581
A; Reference number: Z21581
A; Reference number: T35510
A; Reference number: T35510
A; Reference number: T35510
A; Residues: 1-40 <SEE>
A; Residues: 1-40 <SEE>
A; Residues: T-40 <SEE>
A; Residues: T-40 <SEE>
A; Reperimental source: strain A3(2)
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TPCXSW-------RPWIISNESHCKN--GNSENPIVRPGFIIFNFYTKNDTR 54
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C;Species: Agrobacterium tumefaciens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jun-2001
C;Accession: S21332
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17.8%; Pred. No. 1.5e+02;
Lve 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 48.5; DB 2; 20.0%; Pred. No. 2.2e+02; live 9; Mismatches 18;
                                                                                                                        A, Experimental Source: isolate C3
A, Accession: PQ0854
A, Molecule type: DNA
A, Residues: 1.65 < GOM2>
A, Recession: pQ0853
A, Accession: pQ0853
A, Molecule type: DNA
A, Residues: 1.65 < GO2>
A, Residues: 1.65 < GO2>
C, Superimental Source: strain C6
C, Superimental Source: st
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Best Local Similarity 47.8%;
Matches 11; Conservative
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Matches 14; Conservative
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IY---QVPKC 61
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Best Local Similarity
                                           A; Molecule type: DNA
A; Residues: 1-65 <GOM1>
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A; Residues: 1-59 <PAU>
A; Accession: PQ0851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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hypothetical protein WTH125 - Methanobacterium thermoautotrophicum (strain Delta H) C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1897 #text_change 22-Oct-1999 C; Accession: A69034 R; Smith, Dan. A; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A; Reference number: A69000; MUID:98037514; PMID:9371463 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-62 ATHA A; Cross - references: GB:AB000802; GB:AB000666; NID:92621163; PIDN:AAB84631.1; PID:9262 A; Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BH1388 [imported] - Bacillus halodurans (strain C-125)
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Accession: F83834
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
R; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A; Reference number: A83650; MuID: 20512582; PMID: 11058132
A; Accession: F83834
A; Molecule type: DNA
A; Residues: 1-73 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross.references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05117.1; GSPDB:G
B;Expeximental source: strain C-125
C;Genetics:
A;Gene: BH1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---EPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYTMN 70
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Pred. No. 4.1e+02;
4; Mismatches 28; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.5; DB 2;
Pred. No. 3.5e+02;
2; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             completed: September 29, 2003, 08:49:58
me : 42 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.2%;
Best Local Similarity 22.2%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
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Best Local Similarity
Matches 12; Conserv
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PKK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 PRK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MTH125
A;Start codon: TTG
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                                                                                                                                                                                                                                                                                      RESULT 12
AF2564
hypothetical protein asr8513 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120de C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. pcC 7120
C; Date: 14-Dec-2001 fsequence_revision 14-Dec-2001 ftext_change 09-Dec-2002
C; Accession: AF2564
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Silmpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:2159285; PMID:11759840
A; Status: preliminary
A; Residues: 1-77 < KUR>
A; Accession: AF264
A; Status: preliminary
A; Residues: 1-77 < KUR>
A; Cross-references: GB:AP003604; PIDN:BAB77432.1; PID:G17134876; GSPDB:GN00183
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: asr8513
A; Gene: asr8513
A; Geneences: plasmid
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                                                                                                                                                                                                                 10 KPPTTET---COEDSCYKNIW----TFDNIIRRGCG-----CFTPRGDMPGPYC 51
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                                                     9.3%; Score 47; DB 1; Length 59; 30.5%; Pred. No. 2.9e+02; tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 47; DB 2; Length 77;
33.3%; Pred. No. 3.8e+02;
tive 4; Mismatches 14; Indels
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F;3-22,17-37,39-51,52-57/Disulfide bonds: #status predicted
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31.4%; Pred. No. 2.9e+02;
rative 4; Mismatches 13;
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PCTDAGHERPHRLSSS-----AHKATNLCRRPE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 VKGTKCHPGSPVGFCCPNDGTSSGPYC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 IPGTNKWAGLEKNYCRNPDGDINGPWC 66
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                                                                                Best Local Similarity 30.5 Matches 18; Conservative
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Best Local Similarity
Matches 9; Conserva
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RESULT 14

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September 29, 2003, 08:37:14 ; Search time 22 Seconds (without alignments) 183.832 Million cell updates/sec
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                                                                                                                                                                                                                                US-10-088-548-8
508
1 BQDCMFGNGKGYRGKKATTV......YIMNPRKLFDYCDIPLCASS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10554
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                127863 segs, 47026705 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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	Description	P01481 leiurus	L vibrio c	Q9xzl3 conus texti	andro	Q9p2w3 homo sapien				P28375 dendroaspis	P82815 mesobuthus	Q9gng8 mesobuthus	Q9gyx2 mesobuthus			Q8dc30 vibrio vuln	P01487 leiurus qui	buthus c						-	Q9hps3 halobacteri	-	•	O9ptll gallus gall	~1	m	_	£31	4155	P58328 mesobuthus
SUMMARIES	ei ei	EIO	YO29_VIBCH	CXO6_CONTE	SCX5_ANDMA	GBGD_HUMAN		YP29_VIBPA	SCXB_BUTOC	MAMB_DENJA	SCBK_MESMA	SC15_MESMA	SCA1_MESMA	S482_HYSGI		YG19_VIBVU	SCX3_LEIQU	- 1		٠,	CSPH_SALTY	VG51_BPMD2	NLT2_PRUAR	- 1	RL37_HALN1	CXO1_CONTE	IBB1_COILA	SPY1_CHICK	SCXB_MESMA	Y463_CAUCR	YMXH_BACSU	R332_LISMO	١.	SCX4_MESMA
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	Score	54	54.5	54.5	52.5	49	49	8	48.5	47	47	46.5	46.5	46	46	46	44	44	44	44	43.5	43	43	₹	42.5	•	42	42	42	42	42	ä	41.5	41
	Result No.	٦	7	m	4	S	ø	7	œ	δ	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	36	27	28	29	30	31	32	33

077633 sus scrofa Q9njc8 mesobuthus Q63467 rattus norv Q03191 rattus norv P5890 conus radia P5952 potamon pot Q8pbv2 xanthomonas P5643 andxoctonus Q9pc22 xylella fas P42544 bacteriopha P08072 myxoma viru Q9njc7 mesobuthus		AA. e) Egyptian scorpion). ita; Arachnida; Scorpiones;	oxin V from the scorpion Leiurus s."; channels and inhibits the inactivation thereby blocking neuronal transmission. sed by the venom gland. ALPHA/BETA-SCORPION TOXIN FAMILY. ctri. toxini.	r; Sodium channel inhibitor; Y. Y. Y. Y. T. DD36 CRC64; DB 1; Length 64;	; s 15; Indels 11; Gaps 3; DGDINGPWCYTMNPR 72 	AA.
8.1 75 1 AD10_PIG 8.1 84 1 SC13_MESMA 8.0 81 1 TFF1_RAT 8.0 81 1 TFF3_RAT 8.0 84 1 CXPH_CONRA 7.9 58 1 MT_BOTPO 7.9 64 1 RL32_XANCP 66 1 SCX6_ANDAU 7.9 78 1 YO09_BPIG 7.9 78 1 YO09_BPIG 7.9 78 1 YO09_BPIG 7.9 85 1 GRRA_MYXVL 7.9 85 1 GRRA_MYXVL	ALIGNMENTS	LT 1 SCXS_LENGU STRNDARD; PRT; 64 AA. SCXS_LENGU STRNDARD; PRT; 64 AA. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Leiurus quinquestriatus quinquestriatus (Byptian Bukaryota Metazoa; Arthropoda; Chelicerata; Araciantoidea; Buthidee; Leiurus. NCBL_RAXID-6885; (1) SEQUENCE. MEDLIND-78191225; PubMed-658402; KOPEYAN C., Martinez G., Rochat H.;	of neurot puestriatur puestriatur co sodium (channels, TON Secret TY: Express TY: Express MILY. MILY. Neurotoxi Scorpion.	oit ARI ARI ARI N. CES	4.0%; pred. No. ve 5; MismatcKWAGLEKNYCRKWAGESGYCQWA	STANDARD; PRT; 65
34 35 36 40 37 40.5 39 40.5 40 40 41 40 40 40 40 40 40 40 40 40 40 40 40 40				WW TOXID; Neuron KW Amidation. KW Amidation. FT DISULFID FT DISULFID FT DISULFID FT MOD_RES SQ SEQUENCE (Query Match	Local S hes 16 35	RESULT 2 Y029_VIBCH ID Y029_VIBCH AC Q9KPE1;

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NCBI_TaxID=6494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 KKATTVTGTPC---QEWAAQEPHRHSTFIPGTNK------WAGLEKNYCRNPDGDIN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                  STRAIN=El Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Medelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKITIVKCPRCGTDVEWGEQSPHR----PFCSKQCQMIDFGEWADEEKAIPGAPDMSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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Subraryota: Metazoa, Mollusca: Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54.5; DB 1; Length 65;
Pred. No. 15;
                                                                                                                                                                             3acteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical zinc-binding UPF0243 protein VC2429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: Binds 1 zinc ion (By similarity).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Omega-type conctoxin TxO6 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
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                                                                                                                                                                                                               Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                       Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GPW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 DGW 60
                                                                                                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                               /ibrionaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
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Best Local
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                                                                                                                                                                                                                                                                                                               SIMILARILY).
-!-SUBCELLULAR LOCATION: Secreted (By similarity).
-!-TISSUE SPECIFICITY: Expressed by the venom duct.
-!-SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
                                                                                                                                                                                             Peptides 20:1139-1144(1999).
-!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I-FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.
-I-SUBCRIFULIAR INCORTION: Secreted.
-I-TISSUE SPECIFICITY: EXPRESSED by the venom gland.
-I-SINIBARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Androctonus mauretanicus mauretanicus (Scorpion).
Eukaryota; "Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Androctonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004214; Conotoxin.
Pfam; PF02950; Conotoxin; 1.
Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of ten proteins from the venom of the Moroccan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scorpion Androctonus mauretanicus mauretanicus, six of which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54.5; DB 1; Length 82;
Pred. No. 19;
4; Mismatches 6; Indels
                               TISSUB-Venom duct;
MEDLINE-20037955; PubMed-10573284;
Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
"Conopeptides from Conus striatus and Conus textile by CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMEGA-TYPE CONOTOXIN TXO6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1739D2531B865860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AGLEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin V (AaH V) (AaH5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 AA.
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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Rosso J.P., Rochat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium channel inhibitor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF146359; AAD31919.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9305 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toxic to the mouse.";
Toxicon 23:113-125(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 30.8 les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 AA;
SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6860;
                                                                                                                                                                                                                                                                                                 similarity)
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GRANINE NUCLEOFULE-BINDING PROFEINS (G PROTEINS) ARE INVOLVED AS A MODULACR. OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS: THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GIPALLING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GIPACTOR. INTERACTION.
EFFECTOR INTERACTION.
-!- SUBDNIT: G proteins are composed of 3 units (alpha, beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20145471; Pubmed=10679242;
Inque S., Sano H., Ohta M.;
"Growth suppression of Escherichia coli by induction of expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PDU03.00., SNART; SM00224; GGL; 1.
SNART; SM00224; GGL; 1.
Transducer; Prenylation; Lipoprotein; Multigene family.
LIPID 66 67 REMOVED IN MATURE FORM (BY SIMILARITY).
65 67 REMOVED IN MATURE FORM (BY SIMILARITY).
7049 MW; 080E0C34A8F70327 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Guanine nucleotide-binding protein G(1)/G(S)/G(O) gamma-13 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang L., Shanker Y.G., Dubauskaite J., Zheng J.Z., Yan W., Rosenzweig S., Spielman A.I., Max M., Margolskee R.F.; "Ggammal3 colocalizes with gustducin in taste receptor cells and mediates IP3 responses to bitter denatonium."; Nat. Neurosci. 2:1055-1062(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 1
Pred. No. 64;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY029486; AAK40269.1; -.
EMBL; AB030207; BAA92768.1; -.
EMBL; AB006465; AAK61257.1; -.
EMBL; AF493880; AAM12594.1; -.
EMBL; AL031033; CAB53059.1; ALF_INIT.
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MEDLINE=20040713; PubMed=10570481;
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28-FEB-2003 (Rel. 41, Last sequ
15-SEP-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DiterPro; IPR001770; G-gamma.
Pfam; PF00631; G-gamma; 1.
PRINTS; PR00321; GPROTEING.
ProDom; PD003783; G-gamma; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.6%;
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Matches 13; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:1
MIM; 607298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GBGD MOUSE
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      SOT THE WAR WAS DONE BY BURNESS OF THE SOUTH OF THE SOUTH
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                                                                                                                                                                                                                                                                                            Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Guanine nucleotide-binding protein G(1)/G(S)/G(O) gamma-13 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20040713; PubMed-10570481;
Huang L., Shanker Y.G., Dubauskaite J., Zheng J.Z., Yan W.,
Rosenzweig S., Spielman A.I., Max M., Margolskee R.F.;
"Ggammal3 colocalizes with gustducin in taste receptor cells and
mediates IP3 responses to bitter denatonium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inoue S., Sano H., Ohta M.;
B.:Coli toxicity assay: a novel expression screening method fo
isolation of mammalian genes with membrane-associated domains
binding/ATPase Gonains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 TFIPGIN-----KWAGLEKNYCR--NPDGDINGFWCYTMNPR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 TFFCGRNAYCDDECKKKGGESGYCOWASPYG--NACWCYKLPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3D03A733534CD866 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52.5;
                                                      HSSP; P01484; 1AHO.
InterPro; IPR003614; Knot1.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR0012051; Scorpion_toxinD.
Pfam; PF00537; toxin_3; 1.
PRINTS; PR00284; TOXIN.
ProDom; PD000908; Scorpion_toxinD; 1.
SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21096910; PubMed=11157797;
                                                                                                                                                                                                                                                                                                                                                      BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                   63
36
46
48
64
7301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.4%;
      ALPHA-TOXIN SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Frankland J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                12
16
22
26
64
64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9P2W3; Q9UJJ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Higgs D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GBGD_HUMAN
                                                                                                                                                                                                                                                                                                                           Amidation.
DISULFID
                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GBGD_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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ä

Gaps

64 AA

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 KATTVIGTPC---QEWAAQEPHRHSTFIPGINK------WAGLEKNYCRNPDGDING
                                                                                                                                                                                                                                                                                                                                                           Makino K., Oshima K., Kurokwa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Isasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 561:743-749(2003).

-i. CORACTOR: Binds I zinc ion (By similarity).
-i. SIMILARITY: Belongs to the UPF0243 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buthus occitanus tunetanus (Common European scorpion).
Enkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zinc; Metal-binding; Complete proteome.
                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
AD7939573E9FFEF9 CRC64;
                                                                    15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical zinc-binding UPF0243 protein VP2529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (BY SIMILARITY)
ZINC (BY SIMILARITY)
ZINC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-RIMD 2210633 / Serotype 03:K6;
                                                                                                                                                                                                                                                                                                                                         MEDLINE-22508454; PubMed=12620739;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=84224814; PubMed=6729843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP005081; BAC60792.1; -.
                                             (Rel. 42, Created)
(Rel. 42, Last sequ
(Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
12
28
32
7187 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
  STANDARD;
                                                                                                                                                                       Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00649; -; 1.
Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6871;
                                                                                                                                                                                                                                         NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurotoxin XI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Venom;
                                                5-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCXB_BUTOC
  YP29_VIBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
SCXB_BUTOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                      STRAIN=CSTBL/64; TISSUE=Cerebellum;

XX Kawai J. Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Ehukuishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Asaito T., Okazaki Y., Golobori T., Bono H., Kasikawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Mill D., Hojunga N., Carninci P., de Bonaldo M.F.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Kandone P., Ringy B., Ringwald M., Rodriguez I., Sakamicy D.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ra Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashisaki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AV029485; AAX40268.1; -.
EMBL, AB030194; BAA9757.1; -.
EMBL, AX018778; BAB31403.1; -.
EMBL, AX018778; BAB31403.1; -.
EMBL, AX018778; BAB31403.1; -.
GO; GO:0005834; C:heterotrimeric G-protein complex; IPI.
GO; GO:0007200; P:G-protein signaling, coupled to IP3 second ...; IDA.
InterPro; IPR001770; G-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: GUANNINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSBERRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-EFFECTOR INTERACTION.

-!- SUBUNIT: G proteins are composed of 3 units (alpha, beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART: SMO0224; GGL; 1.
PROSITE; PS50058; G_PROTEIN_GAMMA; 1.
PROSITE; PS50058; G_PROTEIN_GAMMA; 1.
Transducer; Prenylation; Lipoprotein; Multigene family.
LIPID 64 FARNESIL (BY SIMILARITY).
PROPEP 65 67 REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 67;
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
mammalian genes with transmembrane or ATPase domains.";
Biochem. Biophys. Res. Commun. 268:553-561(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 STFIPGTNKWA--GLEKNYCRNPDGDINGPW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 SKTIPELLKWIEDGIPKDPFLNPDLMKNNPW 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD003783; G-gamma; 1
SM00224; GGL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00631; G-gamma; 1.
PRINTS; PR00321; GPROTEING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 13; Conservat
                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
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\$\$\frac{1}{2}\frac{1}{

63

DB 1; Length 64;

:69

25; Indels

65 AA.

ProDom;

```
Martin M.-F., Rochat H.; "Purification of thirteen toxins active on mice from the venom of the North African scorpion Buthus occitanus tunetanus.";
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RESULT 7 YP29_VIBPA

δ g us-10-088-548-8.sep29.rsp

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Arbitragan K.N., Nitthanan S., Sasaki T., Sato K., Cheng B., Srinivasan K.N., Nitthanan S., Sasaki T., Sato K., Cheng B., Srinivasan K.N., Nitthanan S., Sasaki T., Sato K., Cheng B., Srinivasan K.N., Nithanan S., Sasaki T., Sato K., Cheng B., Studional Site of bulkatoxin, an alpha-type sodium channel of the (52) Pukrotion, an alpha-type sodium channel of the (52) Pukrotion (Buthus martensi Karsch) venom: Translet. 494:145-149(2001).

1. FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

1. SUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

1. SUNCTION: Binds to sodium channels and inhibits the inactivation.

2. SUNCTION: Binds to sodium channels and inhibits the inactivation.

2. SINITARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

3. ALPHA-TOXIN SUBFAMILY.

3. InterPro; IPR001219; Neurotoxin.

3. InterPro; IPR001219; Neurotoxin.

3. Prom; PF0057; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 KKATTVIGIPCQE-----WAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGURAL, EXCESS, TROCI, 1.
SWART; SMO505; Knotl, 1.
Neurotoxin; Ionic channel inhibitor; Foxin.
Neurotoxin; 12 63 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 KPPTTET---COEDSCYKNIW-----TFDNIIRRGCG-----CFTPRGDMPGPYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Ebkaryotti Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
NCBL_TAXID=34649;
THE BINDING OF PURIFIED PLATELET FIBRINGEN RECEPTOR GPIIB-IIIA
                                                                                                                                                                                                                                                                                                                                                                       CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 59; 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                             PIR; A42561; T6EE5J.
PDB; 1DRS; 20-DEC-94.
InterPro; IPR003571; Snake_toxin.
Plan; PP000205; Snake_toxin; 1.
Probon; PD000205; Snake_toxin; 1.
PROSITE; PS00272; SNAKE_TOXIN; FALSE_NEG.
Blood coagulation; Cell adhesion; Toxin; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20DDC6A5D9DF9E41 CRC64;
                                                                   -1- TISSUE SPECIFICITY: Expressed by the venom gl: -!- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update) 88-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00284; TOXIN.
Probom; PD000908; Scorpion_toxinL; 1.
                     TO IMMOBILIZED FIBRINGEN. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P82815;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.3
Best Local Similarity 30.5
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                       Blood coagulation;
DISULFID 3
DISULFID 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCBK_MESMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukatoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
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SCHEMENTA
SCHEMENTA
SCHEMENTA
DI 16-OCT
DI 16-OCT
DI 28-FEB
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DI 18-OCT
DI 28-FEB
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                                         of the activated channels, thereby blocking neuronal transmission.

-!- SUBCELULIAR LOCATION: Secreted.
-!- SIBCELULIAR LOCATION: Secreted.
-!- SIBCELULIAR LOCATION: Secreted.
-!- SIBCELULIAR LOCATION: Secreted.
-!- SIBCLENTY: ENTERS of the Alpha/BETA-SCORPION TOXIN FAMILY.

ALPHA-TOXIN SUBFAMILY.

PINIA NTSREB.
R PORT SEED.
R HSSP: PO1464; LANO.
INTERPRO; IPR001219; Neurotoxin.
R InterPro; IPR001219; Neurotoxin.
R Promon: PR000206; Scorpion_toxin.
R PRIMTS: PR00284; TOXIN.
R PROMON: PR000908; Scorpion_toxin.; 1.
R PRAMTS: SM00505; Knotl: 1.
R FAXET: SM00505; Knotl: 1.
W TOXIN: Neurotoxin; Ionic channel inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "IH-NMR assignments and secondary structure of dendroaspin, an RGD-containing glycoprotein IIb-IIIa (alpha IIb-beta 3) antagonist with a neurotoxin fold.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 226:861-868(1994).
                          FUNCTION: Binds to sodium channels and inhibits the inactivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dendroaspis jamesoni kaimosae (Eastern Jameson's mamba).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McDowell R.S., Dennis M.S., Louie A., Shuster M., Mulkerrin M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mambin (Glycoprotein IIb-IIIa antagonist) (Platelet aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mambin, a potent glycoprotein IIb-IIIa antagonist and platelet aggregation inhibitor structurally related to the short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCIURE BY NWR.
MEDLINE-95112851; PubMed-7813476;
Jaseja M., Lu X., Williams J.A., Sutcliffe M.J., Kakkar V.V.,
Parslow R.A., Hyde E.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutcliffe M.J., Jaseja M., Hyde E.I., Lu X., Williams J.A.; "Three-dimensional structure of the RGD-containing neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 48.5; DB 1; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 RHSTFIPGINKWAGL -----EKNYCRNPDGDINGPWCYIM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
992342CEEA431A36 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologue dendroaspin.";
Nat. Struct. Biol. 1:802-812(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR.
MEDLINE=95360732; PubMed=7634091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
MEDLINE=92273586; PubMed=1591238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotoxins.";
Biochemistry 31:4766-4772(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elapidae; Elapinae; Dendroaspis.
NCBI_TaxID=8619;
                                                                                                                                                                                                                                                                                                                                                                                               12 63
16 36
22 46
26 48
65 AA; 7468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor) (Dendroaspin).
  22:279-291(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lazarus R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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Gaps

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28-FEB-2003
28-FEB-2003
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SIGNAL
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                                                                                              09GYX2;
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                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                        5
                                                                                                                                                                                                                                                                                                                                                 TOXICON 38:1653-1661(2000).

-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. This toxin is active against mammals (By similarity).

-!- FUSCHE SPECIFICITY: Expressed by the venom gland.

-!- SIMILARITY: BELONGS.

-!- SIMILARITY: PELONGS.

-!- SIMILARITY: PELONGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00284; TOXIN.
PRINTS; PR0001908; Scorpion_toxinL; 1.
SMART; SM00505; KnotL; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                        Gaps
                                                                                                                                                                                                                                 Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE-2011244; PubMed-10858508;
Zhu S.-Y., Li W.-Y., Zeng X.-C., Liu H., Jiang D.-H., Mao X.;
"Nine novel precursors of Buthus martensil scorpion alpha-toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46.5; DB 1; Length 85;
Pred. No. 1.6e+02;
4; Mismatches 7; Indels
                                                                                             35 RHSTFIPGINKWA-----GLEKNYCRNPDGDINGPWCYTMNPRKL 74
                                                   Length 65;
                                                    Score 4,,
Pred. No. 1e+02,
                                                                                                         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

F2A7D760E7B259DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3312B422EC1C57E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA-NEUROPOXIN TX15.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                   Score 47; DB 1;
                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-neurotoxin TXIS precursor.
                                                                                                                                                                      85 AA.
                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR003614; Knotl.
Interpro: IPR001219; Neurotoxin.
Interpro: IPR001219; Scorpion_toxinL.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF163017; AAG39643.1; -.
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36
46
48
7226 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.28;
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                                                                       12; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
82
83
65
65
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16
22
26
65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                              Similarity
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20
31
35
41
45
85 AA;
                                                                                                                                                                                                                                                                 NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                                                          homologues."
                                                                                                                                                                     SC15_MESMA
DISULFID
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                    DISULFID
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                                                   Query Match
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SIGNAL
                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karsch.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.
This toxin is active against mammals (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00537; toxin_3; 1.
PRINTS; PR00284; TOXIN.
PRODOM: PD009094; Scorpion_toxinL; 1.
SMART; SW00505; Knotl; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                    Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Te J., Chen J., Zuo X., Ji Y.; "Cloning and characterization of cDNA sequences encoding two novel alpha toxin precursors from the Chinese scorpion Buthus martensii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: Expressed by the venom gland.
-i- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
94ED463D6193FFEE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 GYCQWAGVYGNAC------WCYKL-PDKV 74
42 GINKWAGLEKNYCRNPDGDINGPWCYTMNPRKL 74
                                                 53 GYCOWAGVYGNAC------WCYKL-PDKV 74
                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                              85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003614; Knot1.
Interpro; IPR001219; Neurotoxin.
Interpro; IPR002061; Scorpion_toxinL.
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                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF288607; AAG00580.1; -. HSSP; P17728; ILQI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9366 MW;
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                                                                                                                                                                                                                                                                                                                 Alpha toxin 1 precursor.
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85 AA;
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P56854;
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S482_HYSGI
ID S482_H
AC P56854
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CFTPRGDMPGPYC 53
                                                                                                                       54 CRNPDGDINGPWC 66
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                                                                                                                                                                                                                  STANDARD;
                                                                                               Conservative
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Best Local Similarity
Matches 17; Conserv
                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Vibrio vulnificus.
  41
54
45
61 AA;
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=672;
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                               SITE
SEQUENCE
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            DISULFID
  DISULFID
                                                                     Query Match
                                                                                 Local
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YG19_VIBVU
                                                                                             Matches
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                                                                                                                                             MEDIJUE-99017889; PubMed=9799496;
Newcomb R., Szoke B., Palma A., Wang G., Chen X.H., Hopkins W.,
Cong R., Miller J., Urge L., Tarczy-Hornoch K., Loo J.A., Dooley D.J.,
Nadasdi L., Tsien R.W., Lemos J., Miljanich G.;
"Selective peptide antagonist of the class E calcium channel from the
venom of the tarantula Hysterocrates gigas.";
Biochemistry 37:15353-15362(1998),
                                                                                                                                                                                                                                                                                                                                       Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor.
E 41 AA; 4501 MW; C5D3CC96D3AOCFF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=70232598; PubMed=465532;
Joubert F.J., Tallaard N.;
"Some properties and the complete primary structures of two reduced
"Some properties and the complete primary structures of two reduced
and S-carboxymethylated polypeptides (S5C1 and S5C10) from
Dendroaspis jamesoni kaimosae (Jameson's mamba) venom.";
Biochin. Biophys. Acta 579:228-233(1979).
-:- FUNCTION: INHIBITS APP-INDUCED PLATELET AGGREGATION AND INHIBITS
THE BINDING OF PURIFIED PLATELET RIBAINOGEN RECEPTOR GFIIB-IIIA
TO IMMOBILIZED FIBRINOGEN (BY SIMILARITY TO MAMBIN).
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                   -:- SUBCELLULAR LOCATION: Secreted.
-:- TISGUE SPECIFICITY: Expressed by the venom gland.
-:- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dendroaspis jamesoni kaimosae (Eastern Jameson's mamba).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Dendroaspis.
                                                                                                                                                                                                                                             -!- FUNCTION: POTENT AND SELECTIVE BLOCKER OF THE CLASS E CALCIUM
                                                                  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Hysterocrates.
NCBI_TaxID=118972;
                                                                                                                                                                                                                                                                                                                                                                                                         5.
                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 1; Length 41; Pred, No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLUIAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed by the venom gland.
-1- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   48 GLEKNYCRNPDG--DINGPWCYTMNPRKLFDYC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-MUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Toxin S5C1.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF00087; toxin; 1.

ProDom; PD000206; Snake_toxin; 1.

PROSITE; PS00272; SNAKE_TOXIN; FALSE_NEG.
Blood coagulation; Cell adhesion; Toxin.
DISULFID 16 39 BY SIMILARITY.
DISULFID 16 39 SIMILARITY.
                                                        Hysterocrates gigas (African tarantula).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P28375; 1DRS.
InterPro; IPR003571; Snake_toxin.
Pfam; PF00087; toxin; 1.
                                                                                                                                                                                                                                                                                                                                                                               9.1%;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                            HSSP; P56852; 1D1H.
                                          Toxin SNX-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
                                                                                                                                        IISSUE=Venom;
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                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                           Toxin;
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TX51_DENJA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TXITIVXCPQCGTNVEWGEQSPHR----PFCSKKCQMIDFGEWADEENAIPGAPDMSDS
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0
BY SIMILARITY.
BY SIMILARITY.
CELL ATRACHMENT SITE (POTENTIAL).
34825A68D48F7EAA CRC64;
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EMBLAP.

HWARP: WF_00649; -: 1.

Hypothetical protein; 21nc; Metal-binding; Complete proteome.

METAL 12 2 ZINC (BY SIMILARITY).

METAL 28 28 ZINC (BY SIMILARITY).

METAL 32 ZINC (BY SIMILARITY).

METAL 32 ZINC (BY SIMILARITY).

METAL 34 ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong Choy H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 1; Length 64; Pred. No. 1.3e+02;
                                                                                                                                             61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.-:- COFACTOR: Binds 1 zinc ion (By similarity).-:- SIMILARITY: Belongs to the UPF0243 family.
                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical zinc-binding UPF0243 protein VV11619
VV11619.
                                                                                                                                             Score 46; DB 1;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AA.
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE016802; AA010038.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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15-SEP-2003 (Rel. 42, Last sequ
15-SEP-2003 (Rel. 42, Last anno
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September 29, 2003, 08:44:01; Search time 94 Seconds (without alignments) 236.091 Million cell updates/sec
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508
1 BQDCMFGNGKGYRGKKATTV.....YTMNPRKLFDYCDIPLCASS
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                    830525 seqs, 258052604 residues
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9ban9 bos taurus	Q9ukj7 homo sapien	Q9umi2 homo sapien	O9f0v6 azoarcus sp	Q9kpel vibrio chol	Q9ud88 homo sapien	Q9w0y8 drosophila	O8mad3 caenorhabdi	055745 chilo iride	Q8tqr4 saccharomyc	08grv2 oryza sativ	Q9pbp2 xylella fas	089143 visna virus	09blm4 androctonus	Q8add0 human immun	Q8wp57 lutzomyia l
SUMMARIES	ΩI	Q9BGN9	Q9UKJ7	Q9UMI2	Q9F0V6	Q9KPE1	Q9UD88	Q9W0Y8	овмор3	055745	Q8TGR4	Q8GRV2	Q9PBP2	089143	Q9BLM4	Q8ADD0	Q8WP57
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æ	Query Match	25.6	25.1	24.2	11.0	10.7	10.6	10.4	10.1	10.0	8.6	9.7	6.7	9.5	9.5	9.5	9.4
	Score	130	127.5	123	56	54.5	54	53	51.5	51	20	49.5	49.5	48.5	48.5	48.5	48
	Result No.	H	73	3	4	S	ø	7	80	თ	10	11	12	13	14	15	16

Length 75;

Score 130; DB 6; Pred. No. 1.3e-07;

25.68;

Query Match Best Local Similarity

48 9.4 38 5 Q8WRRS 47.5 9.4 59 4 59 2 Q44448 47.5 9.4 59 16 Q8YRJS 47.5 9.4 59 16 Q8YRJS 47.5 9.4 59 3 G7 11 Q9RRJ 47.5 9.3 60 15 Q89J4 47.5 9.3 60 15 Q89J4 47.5 9.3 60 15 Q89J4 46.5 9.2 73 16 Q8YRJS 46.5 9.2 73 16 Q8YRJS 46.5 9.2 86 15 Q89JZ 46.5 9.2 86 15 Q8JZ 46.5 9.2 86 15 Q8Z 47.5 8Z 4	Q8wrr7 lutzomyja u Q8wrr5 lutzomyja i Q8wrr2 lutzomyja i Q8wrr2 lutzomyja m Q8wrr2 lutzomyja m Q8wrr3 lutzomyja m Q8wrr3 lutzomyja w Q8wry w Warw w Q8wry w Q8wry w Warw w Q8wry w Warw w Warw w Q8wry w Warw w Warw w Q8wry w Warw	ALIGNMENTS PRI; 75 AA. reated) ast sequence update) ast annotation update) gment). Craniata; Vertebrata; Eutelecstomi; actyla; Ruminantia; Pecora; Bovoidea; attocyte growth factor in bovine elial cells in vitro."; MBL/GenBank/DDBJ databases. INGLE DOMAINS. 2.
48 9.4 47 9.3 47	Q8WRR7 Q8WRR5 Q8WRR2 Q8WRR4 Q8WRR8 Q8WRR8 Q8WR78 Q9UW3 Q9URD3 Q99146 Q89146 Q89146 Q89146 Q89146 Q8ER13 Q9ER13 Q9ER13 Q9ER13 Q9ER13 Q9ER13 Q9ER14 Q8ER14 Q8ER14 Q8ER16 Q8E	PET; 75 AA Created) Last sequence un Last annotation agment). Craniata; Ver dactyla; Rumina. patocyte growth mehial cells in EMBL/GenBank/DD) RINGLE DOMAINS. 1. 2.
48 9.4 47 9.3 47		17, 23, (Fr. 17, 23, (Fr. 17, 23, (Fr. 17, 28, 28, 28, 28, 28, 28, 28, 28, 28, 28
17 48 9.4 18 48 9.4 19 48 9.4 20 48 9.4 21 48 9.4 22 48 9.4 23 48 9.4 24 9.4 25 47.5 9.4 25 47.5 9.4 26 44.5 9.4 27 47.5 9.4 28 47.5 9.4 29 47.5 9.2 31 47 9.3 31 47 9.3 31 47 9.3 32 46.5 9.2 29 47.5 9.2 31 47.5 9.4 29 0.2 20 0.200000 20 0.200000 20 0.200000 20 0.200000 20 0.2000000 20 0.20000000000	88888888888888888888888888888888888888	MINARY; MBLrel. MBLrel. ABLrel. A factor a, Chora bos. A. A. A. A. A. A. A. A. A.
17 48 18 48 19 48 20 48 21 48 22 48 22 48 23 48 24 48 25 47.5 26 47.5 27 47.5 28 47.5 30 47.5 31 47 31 47 31 47 32 46.5 34 46.5 39 46.5 39 46.5 39 46.5 39 46.5 31 47 47 47 47 47 47 47 47 47 47 47 47 47 4		PRELLI (TIER (TIER
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Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
Rhodocyclaceae; Azoarcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID-666;
                                                                                                                                                                                                                                                                                                            Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56; DB 2; Length 67;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF700742; AAG35589.1; -
EMBL; AF700742; AAG35589.1; -
EMBL; AF700742; AAG35589.1; -
INTERP.P. POOL93; LDR.
FROM PF00037; fer4; 1.
PFAM; PF00037; fer4; 1.
PFAM; PF00037; Iron-sulfur.
SEQUENCE 67 AA; 6997 MW; RESADEAA6FFEL57B CRC64;
                                                                                                                                                                                                                                                        SEQUENCE 53 AA; 5893 MW; 2EB36E715CD40A47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein VC2429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBIRel. 16, Created)
01-MAR-2001 (TrEMBIRel. 16, Last sequence update)
01-MAR-2003 (TrEMBIRel. 23, Last annotation update)
Electron carrier protein ferredoxin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 LEKNYCRNPDGDINGPWCYTMNPRKLFDYCDIPLCA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 INKDICIECEGDFDEPQCLAVCPAG--DACIVPLAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ODCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRH 36
                                                                                                                                                                                                                                                                                                          Score 123; DB 4;
Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AA.
                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                Interpro; IPR000001; Kringle.
Fram, PR00051; Kringle; 1.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; KRINGLE.
PRODUM; PS000031; KR.11, PR051TE; PS000021; KRINGLE.1; FALSE_NEG.
PROSITE; PS00070; KRINGLE.2; 1.
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MEDLINE=21264388; PubMed=11371540;
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                                                                                                                                                                                                                                                                                                               24.2%;
54.3%;
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Best Local Similarity 33.33,
Best Local Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                              19; Conservative
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                                                                                                                                                                                                      Glycoprotein; Kringle. NON_TER 1 1
HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=62928;
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Q9F0V6
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BEDILINE-85023311; PubMed-6148961;

Malinowski D.P., Sadler J.E., Davie E.W.;

Malinowski D.P., Sadler J.E., Davie E.W.;

Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";

Biochemistry 23:4243-4250(1984).

-i- SIMILARIY: CONTAINS I KRINGLE DOMAIN.

EMBL; K02921; AAA60123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21181705; PubMed=11285247;
Ogocelkova M., Kraft H.G., Ehnholm C., Utermann G.;
Single nucleotide polymorphisms in exons of the apo(a) kringles IV
types 6 to 10 domain affect Lp(a) plasma concentrations and have
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Indels
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                  60 AA.
5; Mismatches
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                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein(a) (Fragment) APOA.
Conservative
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01-MAR-2003
19;
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Matches

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Query Match

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Adams W.D., Celniker S.E. II P.W., Hoskins R.A., Galle R.F.,
Ra Amanatides P.G., Scherer S.E., II P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S.., Ashburner W., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Baradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pételffer B.D.,
Ra Bardon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pételffer B.D.,
Ran Abril J.F., Agbayani A., Bn H.-J., Andrews-Pérankoch C., Baldwin D.,
Ballew R.M., Basu B. A., Barman B. P., Brandari D., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bracksten P., Brottier P., Beasley E.M.,
Benos D., Botchan M.R., Bouck J., Escksten P., Brottier P., Brottier P., Borkova D.,
Butris K.C., Busam D.A., Dallke C., Davemport L.B., Davies P.,
Butris K.C., Busam D.A., Dallke C., Davemport L.B., Davies P.,
Butris K.C., Busam D.A., Dallke C., Davemport L.B., Davies P.,
Butris K.C., Busam D.A., Dallke C., Davemport L.B., Davies P.,
Butris K.C., Busam D.A., Bouck J., Broksten D., Dew I., Dietz S.M.,
Bodson K., Doulo E.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Butris K.J., Barvey D., Helman T.J., Hernandez J.R., Retchum K.A.,
Bodson K., Gong F., Gorrell J.H., Gu Z., Genbert W.M., Glasser K.,
RA Hostin D., Bouston K.A., Howland T.J., Well M.-H., Ibegwan C.,
Alali M. Kalush F., Karpen G.H., Rez., Kennison J.A., Ketchum K.A.,
Alali M. Kalush F., Karpen G.H., Rez., Kennison J.M., Marttel B.L., Modinch H., Mobarry C., Morris J., Moshrefi A.,
Rakattel B.L., Molrosh K., Bunghy L., Muzny D.M., Moshrefi A.,
Reinert K., Remignton K., Saunders R.D., Peteler F., Shah H.,
Shue B.C., Siden Kiamos I., Simpson M., Strong R., Shue B.C., Siden Kiamos M., Strong R., Shue B.C., Siden Kiamos J., Shue S., Shue B., Shue B., Save Guodese T., Worley K.C., Wu D., Yeng S., Zhao Y., Smith H.O.,
Reibber S.M., Wooder T., Warley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
Benguence 287:2185-2195(2000).
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A Mannatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D.,
A Barzon J., Besson K.Y., Busan D.A., Carlson J.W., Center A.,
Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V.,
B Champe M., Davenport L.B., Dietz S.M., Dodson K., Farriera S., Frise E.,
Galle R.F., Garg N.S., George R.A., Gonzalez M., Housk J.,
A Galle R.P., Hostin D., Bowland T.J., Ibegwam C., Jalali M.,
A Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M.,
A MIRDHY B., Palson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V.,
A Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittwan G.S.,
A Puri V., Richards S., Scheeler F., Stapleton M., Strong R.,
Syliskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S.,
Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.",
L. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
DT 01-000 (TrEMBLrel. 13, Created)
DT 01-007-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG9971 protein.
3N NaCP60B OR CG9071.
3N Drosophila melanogaster (Fruit fly).
CENSATYOTA: Melazoa, Arthropoda; Hexapoda: Insecta; Pterygota; C Enkaryota; Endopterygota; Diptera; Brachycera; Muscomorpha; C Ephydroidea; Drosophilae; Drosophila.
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MEDLINE=20196006; Pubmed=10731132;
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                                 SEQUENCE FROM N.A.

STRAIN-B. TO. NIG691 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Godson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

Brochand L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-94060120; PubMed-7848387;
Pfaffinger D., Mc Lean J., Scanu A.M.;
"Amplification of human APO(a) kringle 4-37 from blood lymphocyte
                                                                                                                                                                                                                                                                                                   DNA seguence of both chromosomes of the cholera pathogen Vibrio
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
APO(A) KRINGLE 4-37, APO(A) KRINGLE type 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                    TIGK; VCZ429; -.
Interpro; PR005584; DUF329.
Ffam: PF0388, DUF329; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 65 AA; 7397 NW; ZED887CIDID8AD90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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InterPro; IPR000001; Kringle.
Pfam; PF00051; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).
EMBL; AE004312; AAF95572.1;
TIGR; VC2429; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 31.7 hes 20; Conservative
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Matches 7; Conservative
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SEQUENCE
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990D88

RESULT 6 Q9UD88

Query Match

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Q9W0Y8

RESULT 7 Q9W0Y8 ID Q9W0Y

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10; Conservative
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    PRELIMINARY;
                                                                                                                                                                                                                                         Local Similarity
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                                                                                                           NCBI_TaxID=10488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
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Best Local &
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                                                                                                                                                                                                               13 RGKKATTVTGTPCQEW-----AAQEPHRHSTFIPGT-----NKWAGLEKNYC 54
                                                                                                                                                                                       Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Mnofatlo G.J., Lewis S.E., annotation of Drosophila melanogaster genome."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL, RE03465, AR47291.3; ENBL; RE03040529. NacFebs. SEQUENCE 84 AA; 9648 MW; 8668C9865252B777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KDRIPIVSIIESYGIDMPHEHYRYY-----REKNIC-----GISGPICF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels 13;
                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 KATTVIGTPCQEWAAQEPHRHSTFIPGINKWAGLEKNYCRNPDGDINGPWCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 71;
                                                                                                                                                            Length 84;
                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; U28944; AAM81117.1; -- Wormbep; C18A3.10; CE31306. Hyporhetical protein. SEQUENCE 71 AA; 8102 MW; 2C3669D844A93AE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hallsworth K.;
"The sequence of C. elegans cosmid C18A3.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TIEMBLEEL. 22, Created)
01-OCT-2002 (TIEMBLEEL. 22, Last sequence update)
01-MAR-2003 (TIEMBLEEL. 23, Last annotation update)
Hypothetical protein C18A3.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51.5; DB 5;
Pred. No. 1.6e+02;
                                                                                                                                                            Score 53; DB 5; 1
Pred. No. 1.3e+02;
9; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                           71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%;
26.9%;
                                                                                                                                                            10.4%;
25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                         Best_Local Similarity 25.4 Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ci8A3.10.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                  55 RNP 57
                                                                                                                                                                                                                                                                                            RRP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                                                                                                                                                            80
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                           O8MOD3
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MEDLINE=21624570; PubMed=11753363;
Minar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
Miller P., Gerstein M.B., Snyder M.;
"An integrated approach for finding overlooked genes in yeast.";
"An integrated approach for finding overlooked genes in yeast.";
"An integrated approach for finding overlooked genes in yeast.";
"An integrated approach for finding overlooked genes in yeast.";
"Hypothetical protein.

Hypothetical protein.

SEQUENCE 48 AA; 5208 MW; F7C3E1293C8B0202 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 FIPGTNKWAGLEKNYCRNPDGDINGPWCY-----TMNPRKLFDYCDIPLC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Bukaryota, Viidiplantaee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lililopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                         01-UNN-1998 (TIEMBLrel. 06, Created)
01-UNN-1998 (TIEMBLrel. 06, Last sequence update)
01-UNN-1990 (TIEMBLrel. 18, Last annotation update)
Hypothetical 7.5 kDa protein.
Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 3; Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Indels
                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 65 AA; 7526 MW; 1DCD213269477488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hyporhetical 5.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
P0438607.15 protein (B1126F07.15 protein)
P0438607.15 OR B1126F07.15
                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 12;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Sco. 35.7%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AA.
65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 YCRNPDG--DINGPWCYTMNPRKLFDYC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 YCHSRDGRKPGHGPWFGAVGPRQTGEEC 47
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
Bahr U., Tidona C.A., Darai G.;
Virus Genes 0:0-0(1997).
EMBL; AF303741; AAB94456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     10.0%;
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Gaps

17;

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Leroux C., Vuillermoz S., Mornex J.F., Greenland T.; "Genomic heterogeneity in the pol region of ovine lentiviruses obtained from broncholarycolar cells of infected sheep from France."; J. Gen. Virol. 76:1533-1537(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leroux C., Chastang J., Greenland T., Mornex J.F.;
"Genomic heterogeneity of small ruminant lentiviruses: existence of heterogeneous populations in sheep and of the same lentiviral genotypes in sheep and goats.";
Arch. Virol. 142:1125-1137(1997).
EMBL; U35858; AAA78287.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Androctonus australis (Sahara scorpion).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthoidea, Buthidae, Androctonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21211344; PubMed-11311249;
Ceard B., Martin-Eauclaire M.F., Bougis P.E.;
"Evidence for a position-specific deletion as an evolutionary link
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48.5; DB 15; Length 61;
Pred. No. 2.9e+02;
7; Mismatches 18; Indels 11
                                                           DB 16; Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 QEWAA------QEPHRHSTFIPGINKWAGLEKNY-CRNPDGDING
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 61 AA; 7240 MW; C88726FF6FB078B0 CRC64;
 Hypothetical protein; Complete proteome. SEQUENCE 68 AA; 7349 MW; 87902D67E5522F41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TremBirel. 17, Last sequence update) 01-MAR-2003 (TremBirel. 23, Last annotation update) Putative toxin precursor.
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; Retroid viruses; Retroviridae; Lentivirus NCBL_TaxID=11741;
                                                                                                                                   85
                                                                                                                                                         65 WCYTMNPR-----KLFDY-----CDIPLCAS
                                                         Score 49.5; DB 16
Pred. No. 2.5e+02;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AA.
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                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=676;
MEDLINE=95302052; PubMed=7782784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97372948; PubMed=9229003;
                                                                                                                                                                                                                                                                                                                                                              Envelope polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.5%;
                                                           9.78;
                                                                            31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                        Best Local Similarity 31.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                   Visna virus
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SEQUENCE
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                                                              Query Match
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RX Simpson A.J.G. Reinach F.C. Arruda P. Bare E.A., Acencio M., Alves Limbson A.J.G., Raya J.E., Baid G.S., Baptista C.S., Bare G.S., Bare G.S., Baptista C.S., Bare G.S., Bare G.S., Baptista C.S., Bare G.S., Content D.B., Colondo C., Costa R. C. Costa M.C.R., Costa M.C. El-Dorry H., R. Franca J.S., Ferreira V.C.A., Ferro J.A., Franca S.C., Franco M.C., Forbme M., Furlan L.R., Games G.D., Goddman M.H.S., Gomes S.L., Gruber A., Garnier M., Goldman G.H., Coldman M.H.S., Gomes S.L., Kitajima J.P., R. Hopelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramas E.E., Landais M.R., Machado J.A., Marcins E.A.L., Marci
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   5 MFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                  ij
                                     STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                      Score 49.5; DB 10; Length 51; Pred. No. 1.8e+02; 8; Mismatches 27; Indels
                                                                                                                                                                                     Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, clone:B1126F07.";
Cone:B126F07.";
EMBL, AP004398; BAC22372.1;
EMBL, AP005574; BAC22483.1;
                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                     B4EC539E549BFF6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AA.
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                                                                                                                                                                                                                                                                                                     51 AA; 5702 MW;
                                                                                                                                                                                                                                                                                                                                                            29.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein Xf2098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 29.4 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                     STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa.
                                                                                                                                                 SEQUENCE FROM N.A.
                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                            clone:P0438G07."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000
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                                                                                                                                                                                                                                                                                                     SEQUENCE
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 QNCFITKGLGISYGRKKRRQRRKTPQGDPANQDP------IPKQPSSQPRG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                      FEBS Lett. 494:246-248(2001).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
EMBL; AJ308440; CAG37321.1; -.
HSSP; P01484; 1AHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%; Score 48.5; DB 5; Length 85; 31.9%; Pred. No. 4.3e+02; ative 6; Mismatches 15; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 RHSTFIPGTN-----KWAGLEKNYCR--NPDGDINGPWCYTMNPR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. PUTATIVE TOXIN. 4059A69D80E4F090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Tat protein.
TAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
between long- and short-chain scorpion toxins.";
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                                                                                                                                                                           InterPro; IPR003614; Knot1.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001219; Neurotoxin.
Pfam; PF00537; toxin_3; I.
PRINTS; PR00244; TOXIN.
ProDom; PD000909; Scorpio_toxinL; 1.
SMART; SM00505; Knot1; 1.
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20 85
85 AA; 9523 MW;
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Best Local Similarity 31.93
Matches 15; Conservative
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